

FIGURE 1

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer HS-1	CGTGGCCATCCTGGGCAACACCCTG
	G C GG CT
	G
	T
HTRHR	CCTGGGCATTGTAGGCAACATCATGGT
HUMRANTES	CATTGGCCTGGTTGGAAACATCCTGGT
HSBLR1A	CCTGGGCGTGATCGGCAACGTCCTGGT
HUMSOMAT	GGTGGGGCTGGTGGGCAACGCCCTGGT
RNU02083	AGTGGGCCTCTTCGGAAACTTCCTGGT
U00442	GGTGGGCTTAGTGGGCAATTCCCTGGT
HUMNMBR	CGTGGGCTTGCTGGGCAACATCATGCT
HSHM4	GGTGACCATCATCGGCAACATCCTGGT
RATAADRE01	CTTTGCCATCGTGGGCAACATCTTGGT
HUMSSTR3X	GGTGGGCCTGCTGGGTAACTCGCTGGT
HUMC5AAR	GGTGGGAGTGCTGGGCAATGCCCTGGT
HUMRDC1A	CATCGGCATGATTGCCAACTCCGTGGT
HUMOPIODRE	CGTGGCGGTGCTCGGCAACCTCGTGGT
RATA2BAR	GCTGGCAGTGGCGGGCAACGTGCTGGT

09038572-031198

FIGURE 2

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence	TTTGCCATCTGCTGGATGCCCCACAAC
to Primer HS-2	<div> <div>C</div> <div>C</div> <div>TTT</div> <div>C</div> </div> <div> <div>G</div> <div>G</div> </div> <div> <div>T</div> <div>T</div> </div>

HUMSGIR	TTTGCCCTCTGCTGGTTCCCTCTCAAC
HUMBOMB3S	TTTGCCCTCTGCTGGTTGCCAAATCAC
S46950	TTTGCCCTCTGCTGGCTGCCCTACAC
MUSGPCR	TTTGCCCTCGTCTGGTGGCCTCTCAAC
S43387	TTTGCCCTTTTATGGATGCCCTACAGG
RATNEURA	TTTGCCATCTGCTGGCTGCCCTATCAC
RATA1ARA	TTTGCCCTCAGCTGGCTGCCGCTGCAT
HUMOPIODRE	TTTGCCATCTGCTGGCTGCCCTATCAC
HUMNEKAR	TTTGCCATCTGCTGGCTGCCCTACCAC
RATADENREC	TTTGCCTTGTGCTGGCTGCCTTTGTCC
HUMSRI1A	TTTGTATCTGCTGGATGCCTTTCTAC
S8637154	TTTGCTATCTGCTGGCTGCCCTATCAT
RNCGPCR	TTTGCCGCCTGCTGGATGCCTTTTACC
HUMSSTR4Z	TTTGTGCTCTGCTGGATGCCTTTCTAC
RATGNRHA	TTTGCACACTGGTCGAAGCCAGACAAA

09038572.031198

FIGURE 3

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer 3A CTGACCGCTCTIACIACTGACCGATAC
 T T GG GT A C
 G

Primer 3B CTGACCGCTCTIACIACTGACCGATAT
 T T GG GT A C
 G

L11064	CTCACCATGATGAGCGTGGACCGCTAC
L11065	TTGACCATGATGGAGTGTGACCGCTAC
D16349	CTCTGCACCATGAGCGTGGACCGCTAC
X69676	CTGATGCTCGTGAGTATCGACCGCTAC
M35328	CTTACGGCACTGTCAGCTGACAGGTAC
M73482	CTCACTGCCCTCAGCGCCGACAGGTAC
M73481	CTCACGGCGCTCTCGGCAGACAGATAC
L08893	TTAACAATTCTCAGCGCTGACAGATAC
X62933	ATGACCGCCATCGCCGCTGACAGGTAC
X62934	ATGACAACCTGTGGCCTTTGACAGATAC
J05189	ATGACAGCCATTGCAGTGGACAGGTAT
M60786	CTCTGCGCTCTCAGTGTGGACAGGTAC
L04672	CTCACCTGCCTCAGCATTGACCGCTAC
X61496	TTGCTGGCTATCACTGTGGACCGCTAC
X59249	TTGCTGGCCATTGCTGTAGACCGATAC
L09249	CTCACCTGCCTCAGCATTGACCGCTAC
P30731	CTGACAGCTATCGCAGTGGACCGCCAC
M31210	CTCCTCGCCATCGCCATTGAGCGCTAT
U03642	CTCACCGGCCTCAGCTTCGACCGCTAC

09038572-031199
B6T1E0-278E060

FIGURE 4

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer 3C	CTCGCCGCTATIAGCATGGACCGITAC
	G CC G T T

Primer 3D	CTCGCCGCTATIAGCATGGACCGITAT
	G CC G T T

L32840	ATTACCTGCATGAGTGTCGATAGGTAC
X64052	CTCACGTGTCTCAGCATCGATCGCTAC
M90065	CTCACGTGTCTCAGCATCGATCGCTAC
M91464	CTCACGTGTCTCAGCATTGATCGATAC
M88096	CTGGTAGCCATCTCTCTGGAGAGATAT
M99418	CTCGTGGCCATAGCCCTGGAGCGATAC
L04473	CTCGTGGCCATCGCACTGGAGCGGTAC
M73969	CTGGCCTGCATCAGTGTGGACCGTTAC
X65858	TTGGCCTGCATCAGTGTGGACCGTTAC
S46665	CTGGCTACCATTAGTGCCGACCGTTTC
M60626	ATCGCCCTCATTGCTCTGGACCGCTGT

09038572-03198

FIGURE 5

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence TTTACCITCTGTTGGICGCCCTACCACATC
to Primer 6A GT TC T T

Complementary Sequence TTCACCITCTGTTGGICGCCCTACCACATC
to Primer 6B GT TC T T

L11064	TTCGTGGTGTGCTGGGCGCCCATCCACATC
L11065	TTCATCATCTGTTGGACCCCCATTACATC
D16349	TTTATCGTCTGCTGGACCCCCATCCACATC
X69676	TTTGTGCTGTGTTGGGTGCCTTTCCAGATC
M35328	TTTGCCTTCTGCTGGCTCCCCAACCATGTC
M73482	TTCATCTTCTGTTGGTTTCCAAACCACATC
M73481	TTCGCCTTCTGCTGGCTCCCCAATCATGTC
L08893	TTTGCCCTCTGCTGGTTGCCAAATCACCTC
X62933	TTTGCCATCTGCTGGCTGCCCTACCACCTC
X62934	TTCGCCATCTGCTGGCTGCCCTTCCACATC
J05189	TTTGCCATCTGCTGGCTGCCCTATCACGTG
M60786	TTCGCCCTGTGCTGGTTCCCTCTTCACTTA
L04672	TTTGTCACTCTGCTGGCTGCCCTACCACGTG
X61496	TTTGCCGCCTGCTGGATGCCTTTTACCCTC
X59249	TTTGCCTTGTGCTGGCTGCCTTTGTCCATC
L09249	TTTGCCATCTGCTGGCTGCCCTACCACGTG
P30731	TTTGCCCTCTGCTGGTTCCCTCTCAACTGC
M31210	TTCATCGCCTGCTGGGCACCGCTCTTCATC
U03642	TTTGCCCTGTGCTGGATGCCCTACCACCTG

FIGURE 6

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence TTTTTCITTTGCTGGITTCCTACCATG
to Primer 6C CC T G C T T

L32840	TTCATCATTTGCTGGCTTCCCTTCCATGTT
X64052	TTCTTCTTTTCCTGGGTCCCCACCAAATA
M90065	TTCTTCTTTTCCTGGGTCCCCACCAAATA
M91464	TTTTTCTTTTCCTGGATTCCCCACCAAATA
M88096	TTCTTCCTGTGCTGGATGCCCATCTTCAGC
M99418	TTCTTCCTGTGTTGGCTGCCAGTGTACAGC
L04473	TTTTTCTGTGTTGGTTGCCAGTTTATAGT
M73969	TTCCTGCTTTGCTGGCTGCCCTACAACCTG
X65858	TTCCTGCTTTGCTGGCTGCCCTACAACCTG
S46665	TTCTTTATCTTCTGGCTGCCCTATCAGGTG
M60626	TTTTTCTCTGCTGGTCCCCATATCAGGTG

0903857.03198
06TFO.229E060

FIGURE 7

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer T2A

GTCACCAACITGTTTCATCCTCAICCTG

C

AC

GT T

A

HUMGALAREC

ACCACCAACCTGTTTCATCCTCAACCTG

RATADRA1B

CCCACCAACTACTTTATCGTCAACCTG

HUMADRB1

ACCACCAACCTGTTTCATCCTCAACCTG

RABIL8RSB

GTCACCGACGTCTACCTGCTGAACCTG

HUMOPIODRE

GTCACCAACTCCTTCCTCGTGAACCTG

BTSKR

GTGACCAACTACTTCATCGTCAACCTG

HUMSRI2A

ATCACCAACATTTACATCCTCAACCTG

HUMSSTR3Y

GTCACCAACGTCTACATCCTCAACCTG

HUMGARE

GTCACCAACGCCTTCCTCCTCTCACTG

HUMCCKAR

GTCACCAACATCTTCCTCCTCTCCCTG

HUMSHTR

CCCTCCAACACTACCTGATCGTGTCCCTG

HUMD1B

ATGACCAACGTCTTCATCGTGTCTCTG

HUM5HT1E

CCTGCCAACTACCTAATCTGTTCTCTG

HUMD4C

CCCACCAACTCCTTCATCGTGAGCCTG

MMSERO

GCCACCAACTATTTCTGATGTCACTT

RATADRA1A

GTCACCAACTATTTTCATCGTGAACCTG

S57565

CTGACCAATTGCTTCATTGTGTCCCTG

0303857E-031198

FIGURE 8

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence	AACCCITCITCTATTGCTTTITCICT
to Primer T7A	T T C C C G G

HUMGALAREC	AATCCTATCATTTATGCATTTCTCTCT
RATA1ADREC	AACCCCATCGTCTATGCCTTCCGGATC
PIGA2R	AATCCTCTCTTTTATGGCTTTCTGGGG
RAT5HTRTC	AACCCTATCATCTACCCGCTCTTTATG
S58541	AACCCCATCATTTATGCCTTTAATGCT
HUMGRPR	AACCCCTTTGCCCTCTACCTGCTGAGC
MUSGRPBOM	AACCCCTTTGCTCTTTATCTGCTGAGC
RRVT1AIIR	AACCCTCTGTTCTACGGCTTTCTGGGG
HUMADRB1	AACCCCATCATCTACTGCCGCAGCCCC
HSHM4	AACCCCGTGTGCTATGCTCTGTGCAAC
HUMGARE	AACCCCTGGTCTACTGCTTCATGCAC
RATCCKAR	AACCCCATCATCTATTGCTTCATGAAC
S59749	AATCCCATGCTCTACACCTTCGCTGGC
HUMSST28A	AACCCCGTCCTCTACGGCTTCCTCTCG
RNGPROCR	AACCCCATCCTCTACGGCTTCCTCTCC
MUSSSRI1A	AACCCCATACTCTACGGCTTCCTGTCC
HUMA1AADR	AACCCGCTCATCTACCCCTGTTCCAGC
S66181	AACCCGGTTCTCTACGCCTTCCTGGAC
HUMSSTR3Y	AACCCCATCCTTTATGGCTTCCTCTCC

09038572.031199

FIGURE 9

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM1-A2	TGITGGTTATIGGIGTTGTIGGIAA
	CC GC C G

MUSBB2R	TGGTGGTGGTGGTGGTGGTGGGCAA
BTSKR	TGGTGCTGGTGGCTGTGATGGGCAA
BOVEETBR	TGTTTCGTGCTGGGCATCATCGGAAA
HUMNEUYREC	TGATCATTCTTGGTGTCTCTGGAAA
MMSUBKREC	TGGTGCTGGTGGCTGTAACAGGCAA
HUMPGE2R	TGTTTCATCTTCGGGGTGGTGGGCAA
HUMPIR	TGTTTCGTGGCCGGTGTGGTGGGCAA
HSU11053	TGTTTCGTGCTGGGCTTGGTGGGCAA
RRMC3RA	TGGTGATCCTGGCTGTGGTGAGGAA
HUMMR	TGGTTATCCTGGCCGTGGTCAGGAA
MUSGRPBOM	TCATCGTGATAGGTCTTATTGGCAA
RATCHOLREC	TCTTTCTGATGAGTGTTGGCGGAAA
RATCCKAR	TATTCCTTCTCAGTGTGCGGGGGAA

FIGURE 10

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence GCCATACCITGGACAGATACCGAT
to Primer TM3-B2 A T A C G A G

HUMCCKR	GCCATCGCACTGGAGCGGTACAG
HUMCCKBGR	GCCATCGCACTGGAGCGGTACAG
MMGMC5R	GCCATTGCGGTGGACAGGTACA
HUMV2R	GCCATGACGCTGGACCGCCACCG
RATNEURA	GCCATTGCAGTGGACAGGTA
DOGGSTRN	GCCATCGCCCTGGAGCGGATACAG
RAT5HT5A	GCAATAGCTTTGGACCGCTACTGGT
MUSALP2ADA	GCCATTAGTCTGGACCGCTACTGGT
HUMADORA1X	GCAATTGCTGTGGACCGCTACC
HUMOPIODRE	GCCATCGCGGTGGACAGATACA
MUSGRPBOM	GCACTGTCAGCTGACAGGTACAAA
RATCCKAR	GCCATCTCTCTGGAGAGATATGG
HSTRHREC	GCCTTTACCATTGAGAGGTACATA

09038572-031199

FIGURE 11

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM3-C2	CATGGCCGTGGAGAGITACITGGC
	TT C C T A

HUMNK3R	CATTGCGGTGGACAGGTATATGGC
HSMRNAOXY	CATGTCCCTGGACCGCTGCCTGGC
S68242	CATATCGCTGGAGAGATACGGAGC
CFGPCR4	CATCGCTCTGGACAGGTACTGGGC
MMSUBPREC	TGGCCTTTGACAGATACATGGC
HUMOPIODRE	CATCGCGGTGGACAGATACATGGC
HUMGALAREC	ATGTCCGTGGACCGCTACGTGGC
HSS31G	CATTGCCCTGGACAGGTACTGGGC
HUMARB3A	CCTGGCCGTGGACCGCTACCTGGC
HUMHPR	CATGGCCGTGGAGCGCTGCCTGGC
RATCCKAR	CATCTCTCTGGAGAGATATGGCGC

09038572-034196

FIGURE 12

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence	TTTGCCITCTGCTGGATCCCCAAC
to Primer TM6-E2	C G C G TT

HUMNEKAR	TTTGCCATCTGCTGGCTGCCCTAC
HUMSUBPRA	TTCGCCATCTGCTGGCTGCCCTTC
RATSKR	TTTGCCATCTGCTGGCTGCCCTAC
MUSGRPBOM	TTTGCCCTTCTGCTGGCTCCCCAAC
HUMOPIODRE	TTTGCCATCTGCTGGCTGCCCTA
HUMA2XXX	TTTGCCCTCTGCTGGCTGCCCCT
HUMADRBR	TTCACCCTCTGCTGGCTGCCCTTC
CFGPCR8	TTCGCCCCCTCTGTGGCTGCCCCT
HUMETSR	TTTGCCCTCTGCTGGCTTCCCCT
MMNPY1CDS	TTCGCCGTCTGCTGGCTGCCCCT
HSMRNOXY	TTCATCGTGTGCTGGACGCCTTTC
RATCCKAR	TTCTTCCTGTGCTGGATGCCCATC

09038572-031198

FIGURE 13

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM2F18

ARYYTIGCIITIGCNGAY

HUMTSHX	AACCTGGCCTTTGCGGAT
HUMNEKAR	AATCTGGCGCTGGCTGAC
HUMFMLP	AACCTGGCCGTGGCTGAC
HUMINTLEU8	AACCTAGCCTTGGCCGAC
HUMA1AADR	AACCTGGCCGTGGCCGAC
HUMIL8RA	AACCTGGCCTTGGCCGAC
HSDD2	AGCCTCGCAGTGGCCGAC
HUMANTIR	AATTTAGCACTGGCTGAC
HUMSOMAT	AACCTGGCCGTAGCCGAC
HUMEL4REC	AGCTTGGCTGTGGCTGAT
HSTRHREC	AGCCTGGCAGTAGCTGAT
HSU07882	AACCTGGCCTTAGCCGAT

(R = A or G, Y = C or T, N = A, C, G or T, and
I = Inosine)

09038572-031198
B6TTE0-2/8E050

FIGURE 14

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence TTYNNNTNTGYTGGITICCI
to Primer TM6R21

HSBAR	TTCACQCTCTGCTGGCTGCCC
HUMNEKAR	TTTGCCATCTGCTGGCTGCCC
HUMETN1R	TTTGCTCTTTGCTGGTTCCCT
HUMHISH2R	TTCATCATCTGCTGGTTTCCC
HUMA1AADR	TTCGTGCTCTGCTGGTTCCCT
HUMIL8RA	TTCCTGCTTTGCTGGCTGCCC
HUMNMBR	TTCATCTTCTGTTGGTTTCCCT
HUMNKIRX	TTCGCCATCTGCTGGCTGCCC
HUMSUBPRA	TTCGCCATCTGCTGGCTGCCC
HUM5HT1DA	TTTATCATCTGCTGGCTGCCC
HUMPFPR2A	TTCTTCATCTGTTGGTTTCCC
HSDD2	TTCATCATCTGCTGGCTGCCC
HUMNEUYREC	TTTGCACTCTGCTGGCTCCCT
HUM2XXX	TTTGCCCTCTGCTGGCTGCCC
HUMBK2A	TTCATCATCTGCTGGCTGCCC
HUMFMLPX	TTCTTCATCTGTTGGTTTCCC
HUMSSTR3X	TTCGTGCTCTGCTGGATGCCC
HUMCCKR	TTTTTTCTGTGTTGGTTGCCA
HSNEURA	TTTGTGGTCTGCTGGCTGCCC

(Y = C or T, N = A, C, G or T, and I = Inosine)

05038572.031199
DELETED 278E060

FIGURE 15

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer S3A	GCCTGITIAIGATGAGTGTGGAIAGIT
	C G C TC C

HUMGALAREC	CCCTGGCCGCGATGTCCGTGGACCGCT
S70057	GCCTCGTGGCCATCGCACTGGAGCGGT
S67127	ACCTCTGCGCTCTTAGTGTTGACAGGT
S44866	GTCTATGTGCTCTGAGTATTGACAGAT
HUMC5AAR	TCCTGGCCACCATCAGCGCCGACCGCT
HUMANTIR	TACTCACGTGTCTCAGCATTGATCGAT
HUMBK2A	TCCTGATGCTGGTGAGCATCGACCGCT
HSNEURA	ACGTGGCCAGCCTGAGTGTGGAGCGCT
HUMGRPR	CACTCACGGCGCTCTCGGCAGACAGAT
HUMFSRS	GCCTGACAGTCATGAGCGTGGACCGCT
HUMIL8RA	TGTTGGCCTGCATCAGTGTGGACCGTT
HUMNEKAR	CCATGACCGCCATTGCTGCCGACAGGT

FIGURE 16

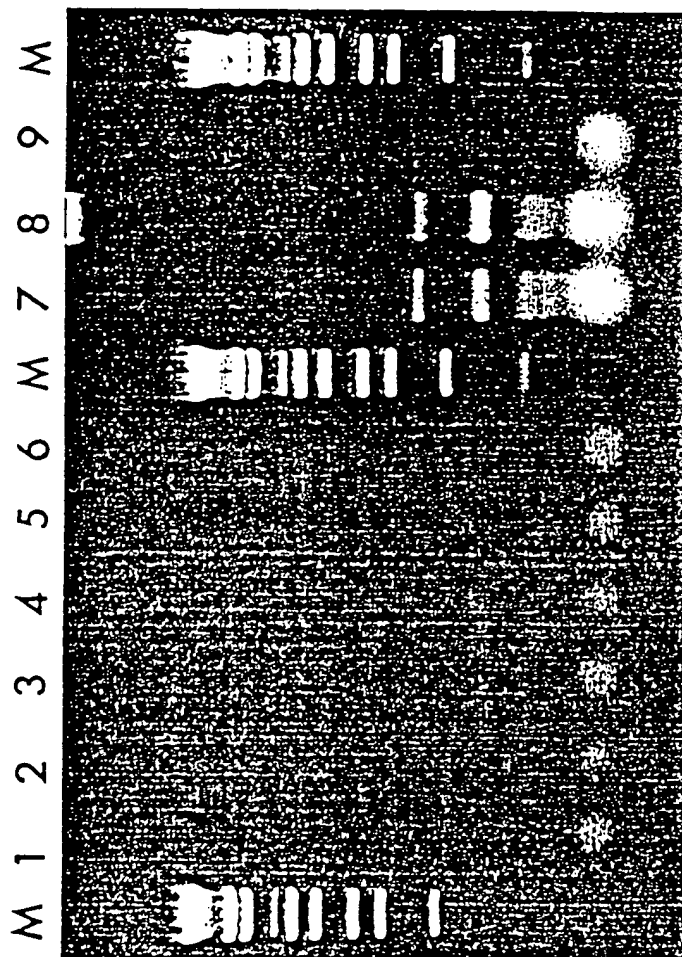
COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence TGGITICCTACCACITATCAICATC
to Primer S6A T T GG GT

HUMGALAREC	TGGCTGCCGCACCACATCATCCATCTC
S70057	TGGTTGCCAGTTTATAGTGCCAACACG
S67127	TGGTTCCCTCTTCATTTAAGCCGTATA
S44866	TGGCTTCCCCTTCACCTCAGCAGGATT
HUMC5AAR	TGGTTGCCCTACCAGGTGACGGGGATA
HUMANTIR	TGGATTCCCCACCAAATATTCACTTTT
HUMBK2A	TGGCTGCCCTTCCAGATCAGCACCTTC
HSNEURA	TGGACTCCGTTCTCTATGACTTCTAC
HUMGRPR	TGGCTCCCCAATCATGTCATCTACCTG
HUMFSRS	TGGCTGCCCTTCTTCACCGTCAACATC
HUMIL8RA	TGGCTGCCCTACAACCTGGTCCTGCTG
HUMNEKAR	TGGCTGCCCTACCACCTCTACTTCATC

09038572-03198

FIGURE 17



	10	20	30	40	50
A58-T7-2	GTGGGCATGGTGGCAACCCCTGGTCA	TCTTTCGTGATCCTTCGCTACGC			
HUMSOMAT	X:::	:::::	:::::	:::::	:::::
A58-T7-2	GTGGGGCTGGTGGGCAACGCCCTGGTCA	TCTTTCGTGATCCTTCGCTACGC			
HUMSOMAT	285	295	305	315	325
A58-T7-2	60	70	80	90	100
HUMSOMAT	CAAGATGAAGACGGCTACCAACATCTAC	CTGCTCAACCTGGCCGTAGCCG			
A58-T7-2	335	345	355	365	375
HUMSOMAT	110	120	130	140	150
A58-T7-2	ACGAGCTCTTCATGCTGAGCGTGCCCTT	CGTGCGCTCGTCGGCCGCCCTG			
HUMSOMAT	385	395	405	415	425
A58-T7-2	160	170	180	190	200
HUMSOMAT	CGCCACTGGCCCTTCGGCTCCCGTGCTG	TGCGCGCGGTGCTCAGCGTCGA			
A58-T7-2	435	445	455	465	475
HUMSOMAT	210	220	230	240	
A58-T7-2	CGGCC	TCAACATGTTACCA	CGGTCTTCTG	TCTCAACCGTGCTCAGCGT	
HUMSOMAT	485	495	505	515	
A58-T7-2	CGGCC	TCAACATGTTACCA	CGGTCTTCTG	TCTCAACCGTGCTCAGCGT	
HUMSOMAT					X

[illegible]

	10	20	30	40	50
57-A-2	<u>GTGGGCATGCTGGGCCAACCTCCTGGAAGGCAGTCGCCGAGGTGGCCGGTT</u>				
HUMDRD5A	X:::	:	:	:	:
	424	434	444	454	
	60	70	80	90	100
57-A-2	ACTGGCCCTTTTGGAGCGTTCTGCGACGTCTGGGTGGCCCTTCGACATCATG				
HUMDRD5A	ACTGGCCCTTTTGGAGCGTTCTGCGACGTCTGGGTGGCCCTTCGACATCATG				
	464	474	484	494	504
	110	120	130	140	150
57-A-2	TGCTCCACTGCCTCCATCCTGAACCTGTGCGTCATCAGCGTGGACCGCTA				
HUMDRD5A	TGCTCCACTGCCTCCATCCTGAACCTGTGCGTCATCAGCGTGGACCGCTA				
	514	524	534	544	554
	160	170	180	190	200
57-A-2	CTGGGCCATCTCCAGGCCCTTCCGCTACAAGCGCAAGATGACTCAGCGCA				
HUMDRD5A	CTGGGCCATCTCCAGGCCCTTCCGCTACAAGCGCAAGATGACTCAGCGCA				
	564	574	584	594	604
	210	220	230	240	250
57-A-2	TGGCCTTGGTTCATGGTTCGGCTGGCATGGACCTTGTCATCCTCATCTCC				
HUMDRD5A	TGGCCTTGGTTCATGGTTCGGCTGGCATGGACCTTGTCATCCTCATCTCC				
	614	624	634	644	654
	260	270	280	290	300
57-A-2	TTCATTCCGGTCCAGGTCAA CTGGGACAGGGACCAGGCGGGCTCTTGGGG				
HUMDRD5A	TTCATTCCGGTCCAGGTCAA CTGGCACAGGGACCAGGCGGCCTCTTGGGG				
	664	674	684	694	704
	310				
57-A-2	GGGGCTGGACCTGCCAAA				
HUMDRD5A	CGGGCTGGACCTGCCAAA				
	714	724			

B54	10	20	30	40	50
	<u>GTGGGCATCGTGGGCAACATCCTTGGTCATATTTCGTGATCCTACGCTATGC</u>				
RNU04738	X: ::::	: :: ::	: :: ::	: ::::	: ::::
	GTGGGCCCTGGTAGGAAACGCCCTGGTCATATTTCGTGATCCTACGCTATGC				
	233	243	253	263	273
B54	60	70	80	90	100
	CAAAATGAAGACAGCCACCAACATCTACCTGCTCAACCTGGCCGTCGCTG				
RNU04738	: ::::				
	CAAAATGAAGACAGCCACCAACATCTACCTGCTCAACCTGGCCGTCGCTG				
	283	293	303	313	323
B54	110	120	130	140	150
	ATGAGCTCTTCATGCTCAGTGTGCCATTGTGGCCTCGGGGGCTGCCCTG				
RNU04738	: ::::				
	ATGAGCTCTTCATGCTCAGTGTGCCATTGTGGCCTCGGGGGCTGCCCTG				
	333	343	353	363	373
B54	160	170	180		
	CGCCACTGGCCGTTCCGGGGCGGTGCTGTGCCGC				
RNU04738	: ::::				
	CGCCACTGGCCGTTCCGGGGCGGTGCTGTGCCGC				
	383	393	403		

	9	18	27	36	45	54
GTG GGC ATG GTG GGC AAC GTC CTC CTG GTG CTG ATC GCG CCG GTG CGC						
Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg						
CTG CAC AAC GTG ACG AAC TTC CTC CTC ATC GGC AAC CTG GCC TTG TCC GAG CCG GTG	63	72	81	90	99	108
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu						
ATG TGC ACC GCC TGC GTG CCG CTC CCG CTC ACG CTG GCC TAT GAG CCA CCG GGC	117	126	135	144	153	162
Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly						
TGG GTG TTC GGC GGC GGC CTG TGC CAC CAC CTG GTG TTC TTC CTG CAG CCG GTC ACC	171	180	189	198	207	216
Trp Val Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr						
GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ACC ATC GAA GTG GAC CCG TAC GTC GGT	225	234	243	252	261	270
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr						
GCT GGT GCA CCC GCT GAG GCG GCG CAT 3'	279	288	297			
Ala Gly Ala Pro Ala Glu Ala Gly His						

FIGURE 23

5'	GGC	CTG	CTG	CTG	GTC	ACC	TAC	CTG	CTC	CCT	CTG	CTG	ATC	CTC	CTG	TCT	TAC	54
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Gly	Leu	Leu	Leu	Val	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr
	63	GTC	CGG	GTC	TCA	GTC	CTC	CGC	AAC	CCG	GTG	GTG	CCG	GTC	TGC	GTG	ACC	CAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Pro	Val	Val	Pro	Val	Cys	Val	Thr	Gln
	117	AGC	CAG	GCC	GAC	TGG	GAC	CGC	GCT	CGG	CGC	CGG	ACC	TTC	TGC	TTC	CTG	GTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Ser	Gln	Ala	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val
	171	GTG	GTC	GTG	GTG	TTC	GCC	ATC	TGC	TGG	TTC	CCT	TAC	TAC				
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Val	Val	Val	Val	Val	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Tyr	Tyr				

FIGURE 24

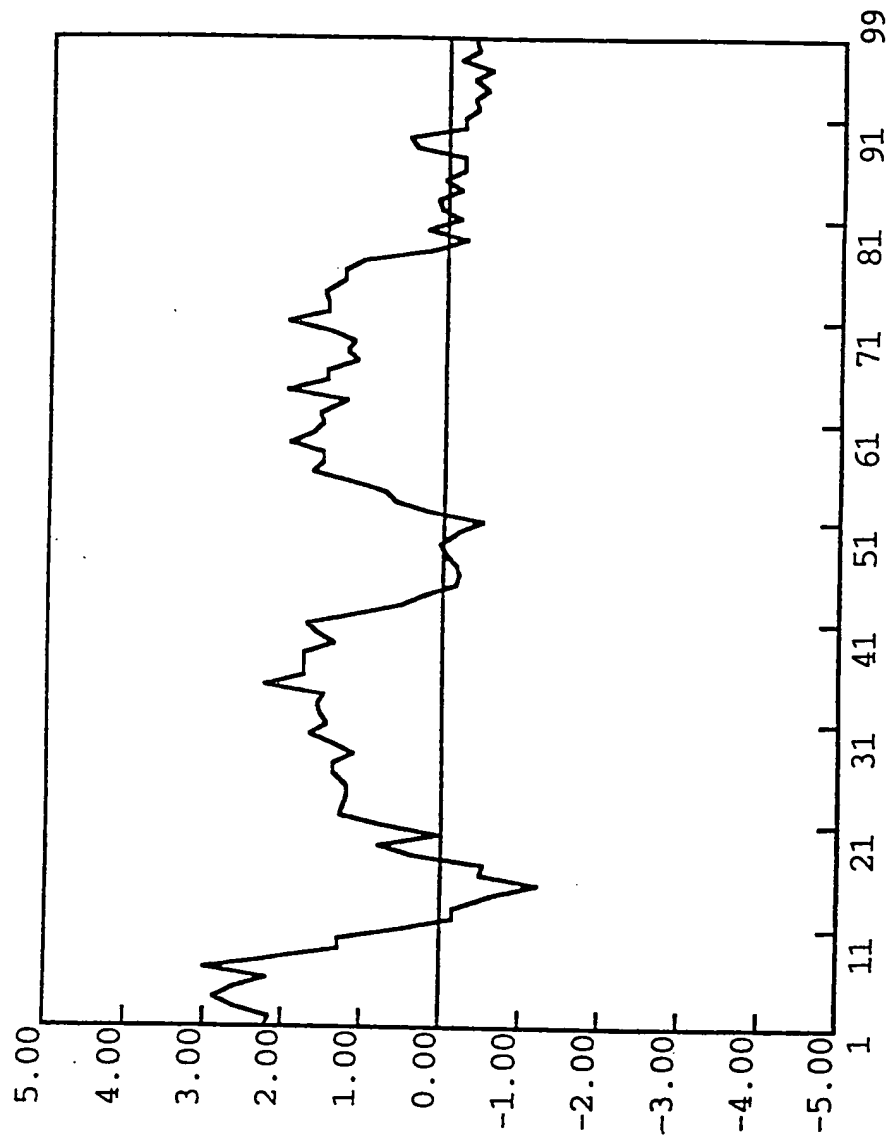


FIGURE 25

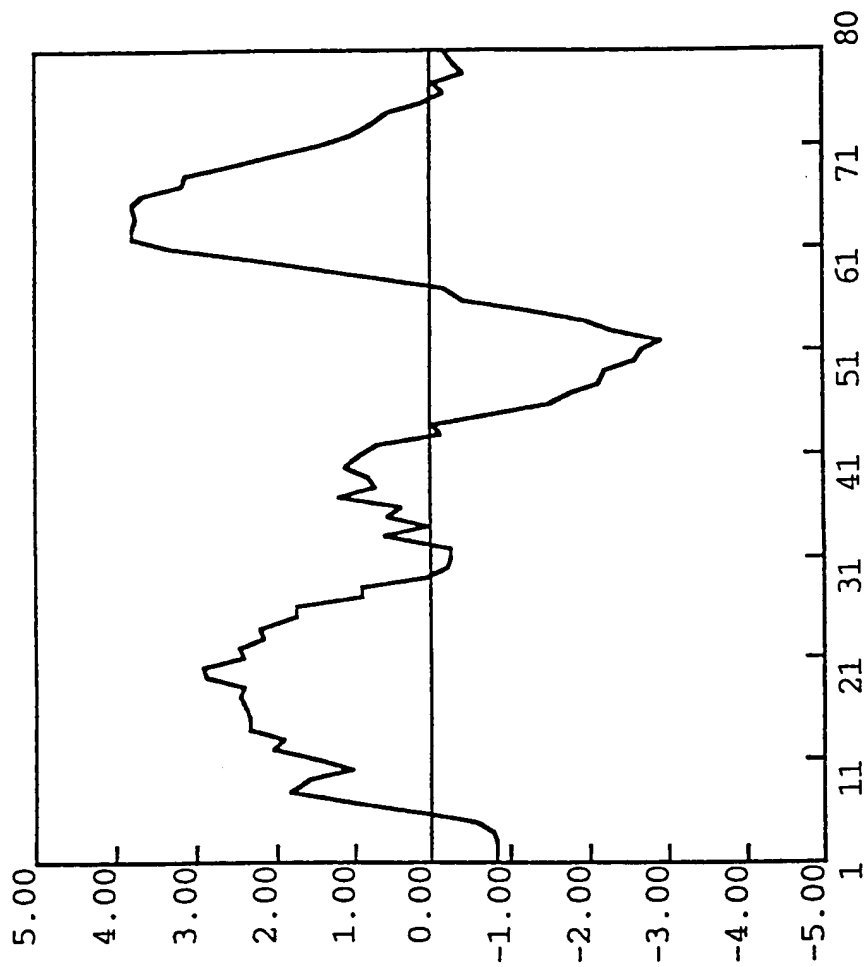


FIGURE 26

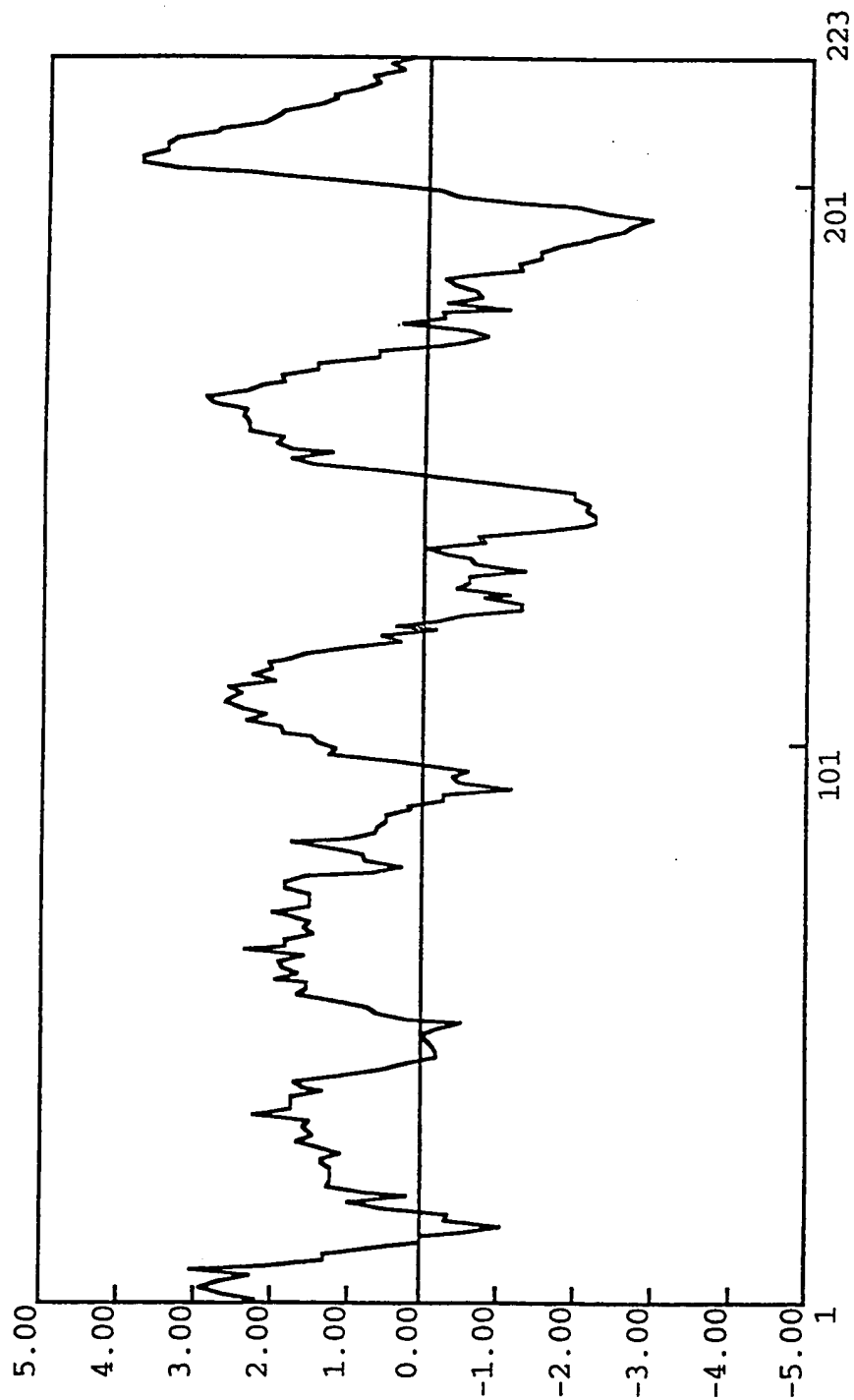
p19P2	1	VGMVGNVLLV	LV	IARVRLH	NVTNFLIGNL	ALSDVLMCTA	CVPLTLAYAF	50
S12863	1	LGVSGLAL	I	ILKQKEMR	NVTNILLIVNL	SFSDILLVAVM	CLPFTFVYTL	50
		10	20	30	40	50		
p19P2	51	EPRGWVFGGG	LCHLVFFLQIP	VTVYVSVFTL	TTTEVDRYVG	AGAPAEAGH	100	
S12863	51	MDH-WVFGET	MCKLNPEVQC	VSITVSIIESL	VLIIVERHQL	IINPRGWRPN	100	
		60	70	80	90	100		
p19P2	101		120	130	140	150		
S12863	101	NRHAYIGITV	IWVLAVASSL	PFVIYQILTD	EPFQNVSLAA	FKDKYVCFDK	150	
		110	120	130	140	150		
p19P2	151	GLLV	TYLLPLLVIL	LS-----Y	VRSVKLRNPV	VPVCVTQSQA	200	
S12863	151	FPSDSHRLSY	TTLLLVLLQYF	GPLCFIFICY	FKIYIRLKR	NNMMDKIRDS	200	
		160	170	180	190	200		
p19P2	201	DWDRARRRRRT	FCLLVVVVVV	FAICWLPPY	250	
S12863	201	KYRSSETKRI	NVMLLSIVVA	FAVCWLPLT	250	
		210	220	230	240	250		

FIGURE 27

5'	GTG	GGC	ATG	GTG	GGC	AAC	ATC	CTG	CTG	GTG	CTG	GTG	ATC	GCG	CGG	GTG	CGC	CGG	54
	Val	Gly	Met	Val	Gly	Asn	Ile	Leu	Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	
	CTG	TAC	AAC	GTG	ACG	AAT	TTC	CTC	ATC	GGC	AAC	CTG	GCC	TTG	TCC	GAC	GTG	CTC	108
	Leu	Tyr	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	
	ATG	TGC	ACC	GCC	TGC	GTG	CCG	CTC	ACG	CTG	GCC	TAT	GCC	TTC	GAG	CCA	CGC	GGC	162
	Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	
	TGG	GTG	TTC	GGC	GGC	GGC	CTG	TGC	CAC	CTG	GTC	TTC	TTC	CTG	CAG	GCG	GTC	ACC	216
	Trp	Val	Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Ala	Val	Thr	
	GTC	TAT	GTG	TGC	GTG	TTC	ACG	CTC	ACC	ACC	ATC	GCA	GTG	GAC	CGC	TAC	GTC	GTG	270
	Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	
	CTG	GTG	CAC	CCG	CTG	AGG	CGG	CGC	ATC	TCG	CTG	CGC	CTC	AGC	GCC	TAC	GCT	GTG	324
	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	
	CTG	GCC	ATC	TGG	GTG	CTG	TCC	GCG	GTG	CTG	GCG	CTG	CCC	GCC	GCC	GTG	CAC	ACC	378
	Leu	Ala	Ile	Trp	Val	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	
	TAT	CAC	GTG	GAG	CTC	AAG	CCG	CAC	GAC	GTG	CGC	CTC	TGC	GAG	GAG	TTC	TGG	GGC	432
	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val	Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly	
	TCC	CAG	GAG	CGC	CAG	CGC	CAG	CTC	TAC	GCC	TGG	GGG	CTG	CTG	CTG	GTC	ACC	TAC	486
	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Val	Thr	Tyr	
	CTG	CTC	CCT	CTG	CTG	GTC	ATC	CTC	CTG	TCT	TAC	GCC	CGG	GTG	TCA	GTG	AAG	CTC	540
	Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr	Ala	Arg	Val	Ser	Val	Lys	Leu	
	CGC	AAC	CGC	GTG	GTG	CCG	GGC	CGC	GTG	ACC	CAG	AGC	CAG	GCC	GAC	TGG	GAC	CGC	594
	Arg	Asn	Arg	Val	Val	Pro	Gly	Arg	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	
	GCT	CGG	CGC	CGG	CGC	ACC	TTC	TGC	TTG	CTG	GTG	GTG	GTC	GTG	GTG	GTG	TTC	ACC	648
	Ala	Arg	Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	
	CTC	TGC	TGG	CTG	CCC	TTC	TTC	3'											
	Leu	Cys	Trp	Leu	Pro	Phe	Phe												

05038572-031198

FIGURE 28



5'	10	19	28	37	46	55
GTG GGC ATG CTG GGC AAC GCC CTG	Val Cys His Val Ile Phe Lys Asn Gln Arg					
ATG CAC TCG GCC ACC AGC CTC TTC ATC	91	100				109
Met His Ser Ala Thr Ser Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met						
ATC ACG CTG CTC AAC ACC CCC TTC ACT TTG GTT CGC	145	154				163
Ile Thr Leu Leu Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp						
ATA TTT GGG AAG GGC ATG TGC CAT	190	208				217
Ile Phe Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu						
CAC GTC TCA GCA CTG ACA 3'	235					
His Val Ser Ala Leu Thr						

[illegible]

FIGURE 31

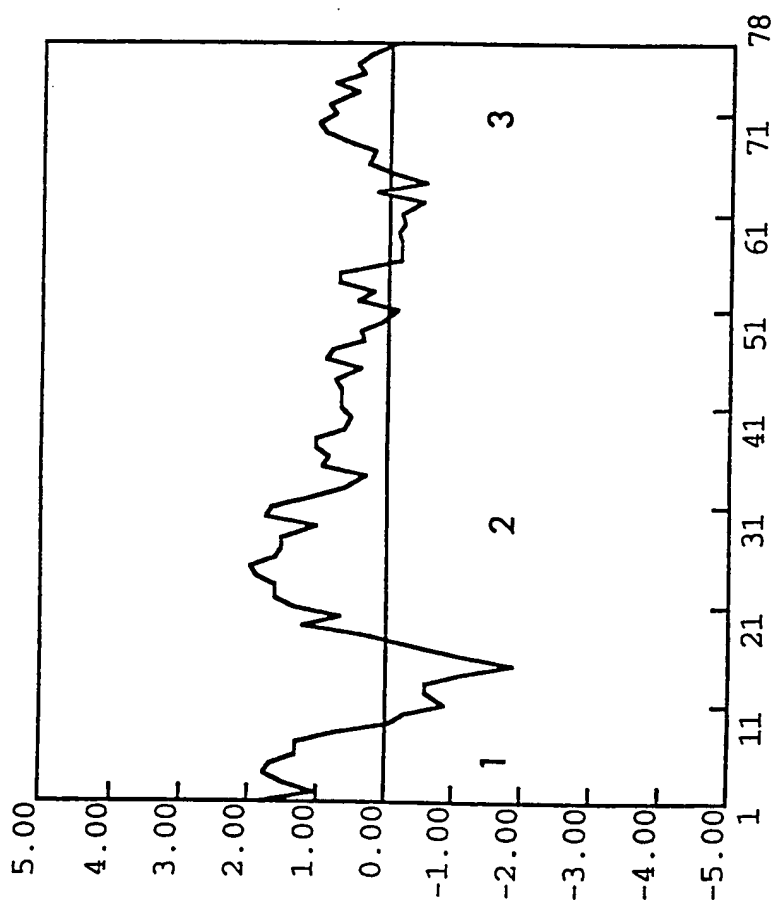


FIGURE 32

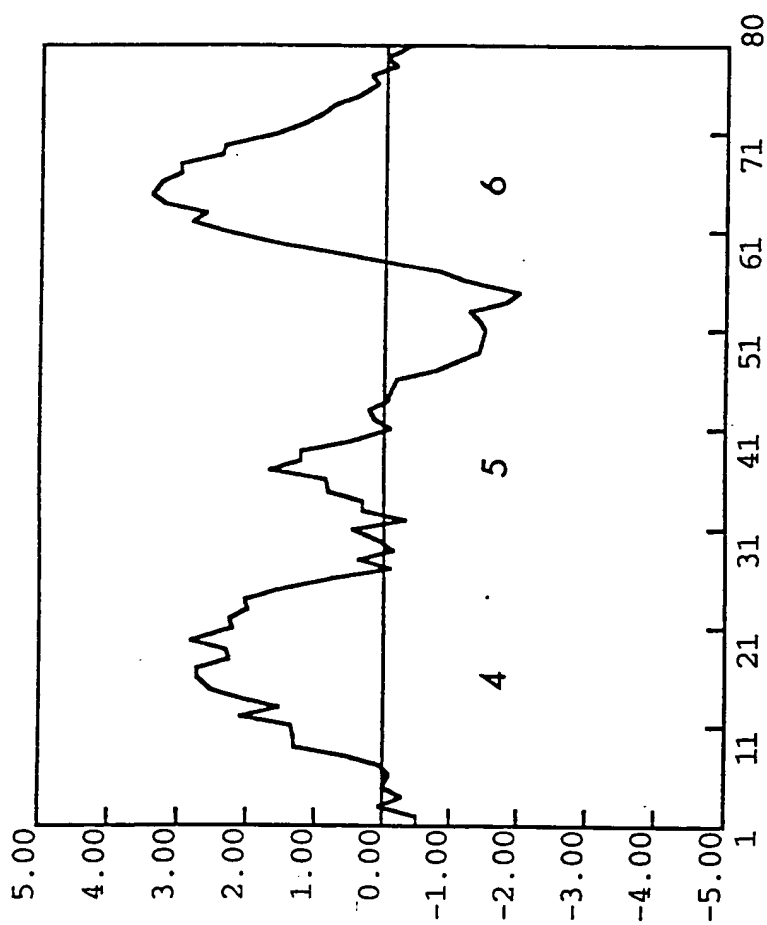


FIGURE 33

p63A2	1	10	20	30	40	50
P30731	1	VCHVTEKNQR	MHSATSLFIV	NLAADIMIT	LINTPFTEVR	FVNSTWIFGK
	1	VCHVTEKNQR	MHSATSLFIV	NLAADIMIT	LINTPFTEVR	FVNSTWIFGK
p63A2	51	60	70	80	90	100
P30731	51	GMCHVSRFAQ	YCSLHVSAIT	LTATAVDRHQ	VIMHPLKPRI	SITKGVIIYA
	51	GMCHVSRFAQ	YCSLHVSAIT	LTATAVDRHQ	VIMHPLKPRI	SITKGVIIYA
p63A2	101	110	120	130	140	150
P30731	101	VIWVMATFFS	LPHATCQKLF	TFKYSEDIVR	SLCLPDFPER	ADLEFWKNLDL
	101	VIWVMATFFS	LPHATCQKLF	TFKYSEDIVR	SLCLPDFPER	ADLEFWKNLDL
p63A2	151	160	170	180	190	200
P30731	151	PTFTLLNI LP	LLTISVAVVR	VTKKLWLCNM	TVDVTTTEQYF	ALRPKPKKTI
	151	ATFTLLNI LP	LFITISVAVAR	VAKKLWLCNT	IGDVTTTEQYL	ALRRKPKKTI
p63A2	201	210	220	230	240	250
P30731	201	KHEMLAVVVL
	201	KHEMLAVVVL

FIGURE 34

1	CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGGCCAGCAGAAATT	60
1		1
61	CTGCCCCCTTCTTCCCGGAGTGCTTTCCCGCTCTCCAAACCCCACTCCCAGGTGGCCATG	120
1	Met	1
121	GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTCTGGGCTGCCGCCGGCG	180
1	AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla	21
181	GTCACAACCTCCCGCCAACCAGAGCGCAGAGGCTCGGGCGGCAACGGGTGGTGGCTGGC	240
21	ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly	41
241	GCGGACGCTCCAGCCGTCACGCCCTTCCAGAGCCTGCAGCTGGTGATCAGCTGAAGGGG	300
41	AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly	61
301	CTGATCGTGCTGCTCTACAGCGTCTGGTGGTGGTGGGGCTGGTGGGCAACTGCCTGCTG	360
61	LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTGATCGCGGGGTGCGCCGCTGCACAACGTGACGAACCTCCTCATCGGCAAC	420
81	ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTGTCCGACGTGCTCATGTGCACCGCTGCGTGCCGCTCACGCTGGCCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTGAGCCACGCGGCTGGGTGTTCCGCGCGGCCTGTGCCACCTGGTCTTCTTCTGTCAG	540
121	PheGluProArgGlyTrpValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTCAACGCTCTATGTGTGCGGTTCACGCTACCAACCATCGCAGTGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
601	GTGCTGGTGACCCGCTGAGGCGGCGCATCTCGCTGCGCCTCAGCGCTACGCTGTGCTG	660
161	ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
661	GCCATCTGGGCGCTGTCCGCGGTGCTGGCGCTGCCGCGCGCTGCACACCTATCACGTG	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGACGACGTGCGCCTCTGCGAGGAGTTCTGGGGCTCCCAGGAGCGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCTGGGGCTGCTGCTGGTCACTACCTGCTCCCTCTGCTGGTCACTC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241
841	CTCCTGTCTTACGTCCGGGTGTCAGTGAAGCTCCGCAACCGCTGGTGGCGGGCTGCGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGGCCGACTGGGACCGCGCTCGGCGCGGCGCACCTTCTGCTTGGTGGT	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTCTGGTGGTGTTCGCCGCTGCTGGCTGCGCTGCACGCTTCAACCTGCTGCGG	1020
281	ValValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCCACGCCATCGACCTTACGCCCTTGGGCTGGTGCAGCTGCTCTGCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTCGCCATGAGTTCCGGCTGCTACAACCCCTTCATCTACGCTGGCTGCACGACAGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCGCGAGGAGCTGCGCAACTGTTGGTGGCTTGGCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAAATATGACCGTCAGCGTGGTCATCTGATGCCACTTAGCCAGGCCTTGGTCAAGGAGC	1260
361	GlnAsnMetThrValSerValValIle***	371
1261	TCCACTTCAACTGGCCTCCTAGGGCACCCTCGAGGTCAATCTGGTGGCTTATTCTCAGCA	1320
371		371
1321	CCAGAGCTAGC	1331
371		371

09038572-031106

FIGURE 35

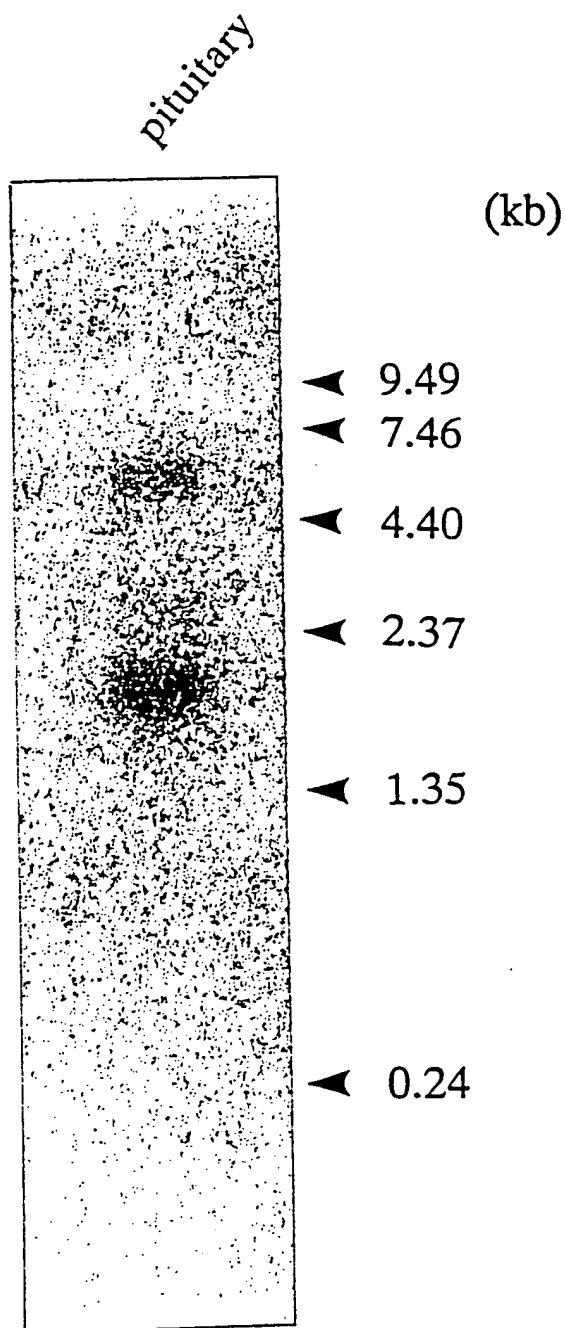


FIGURE 36

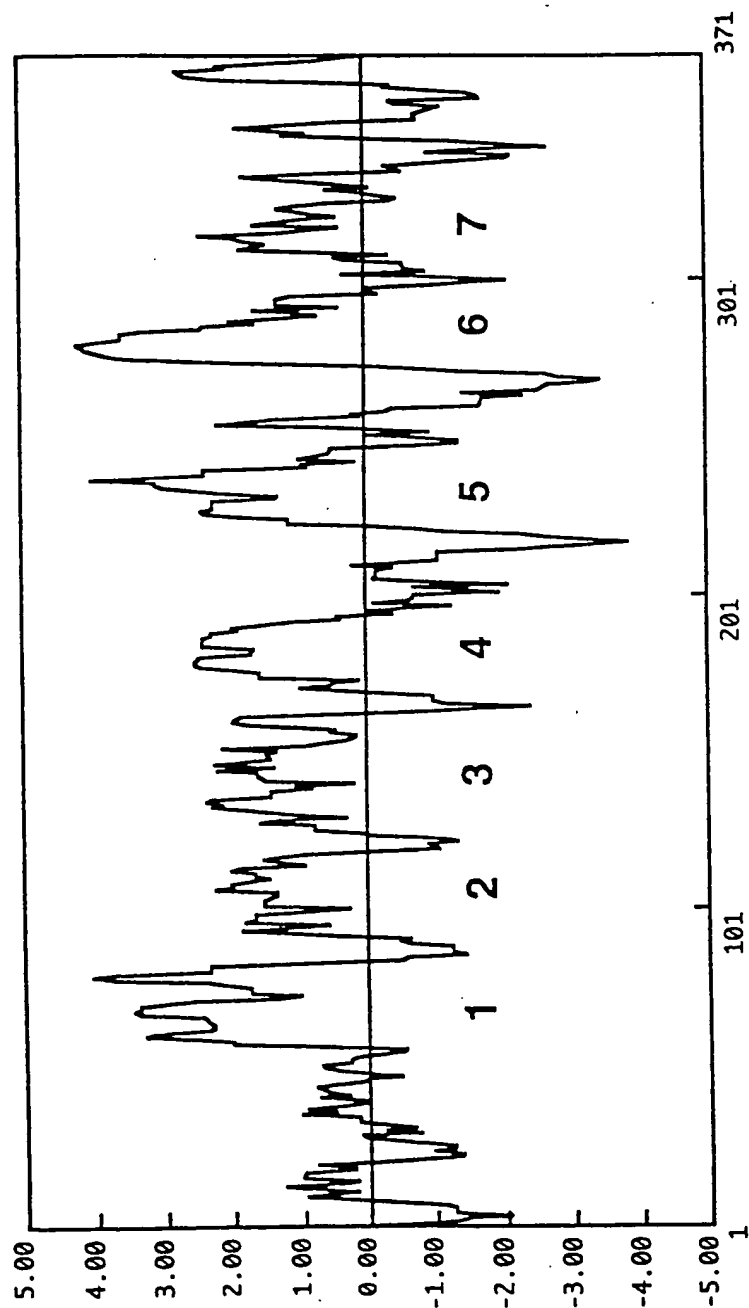


FIGURE 38

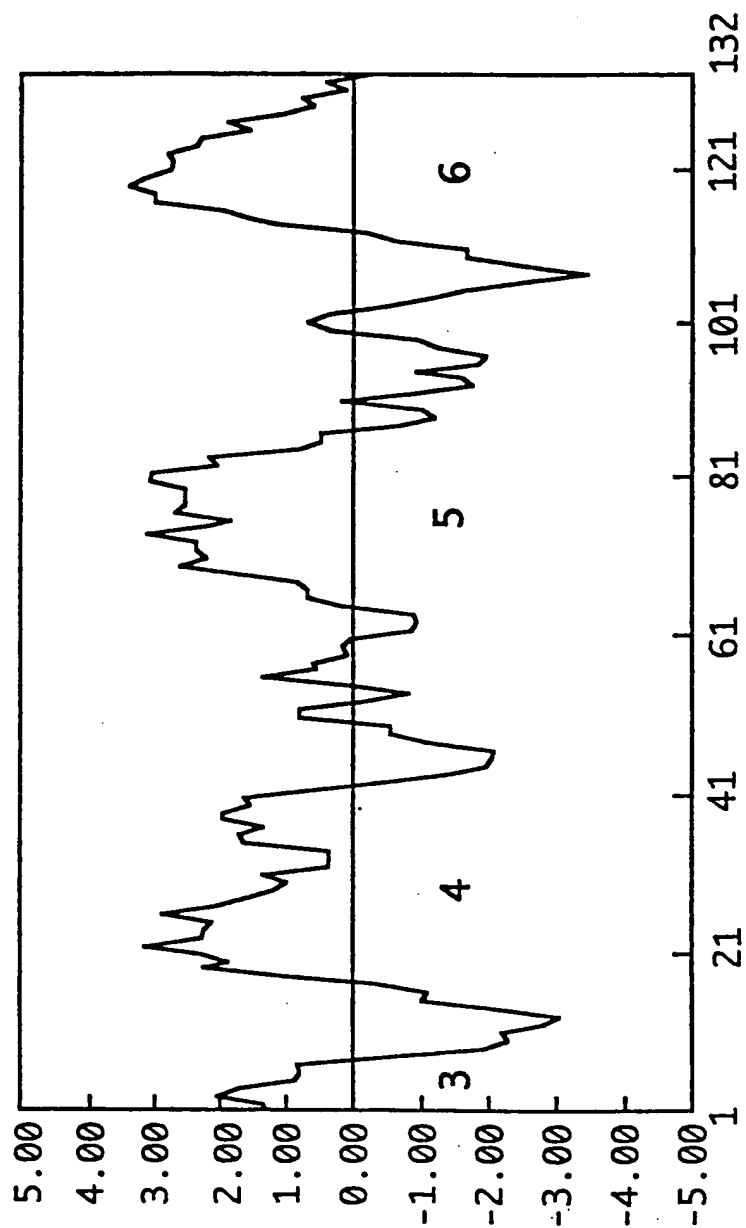


FIGURE 39

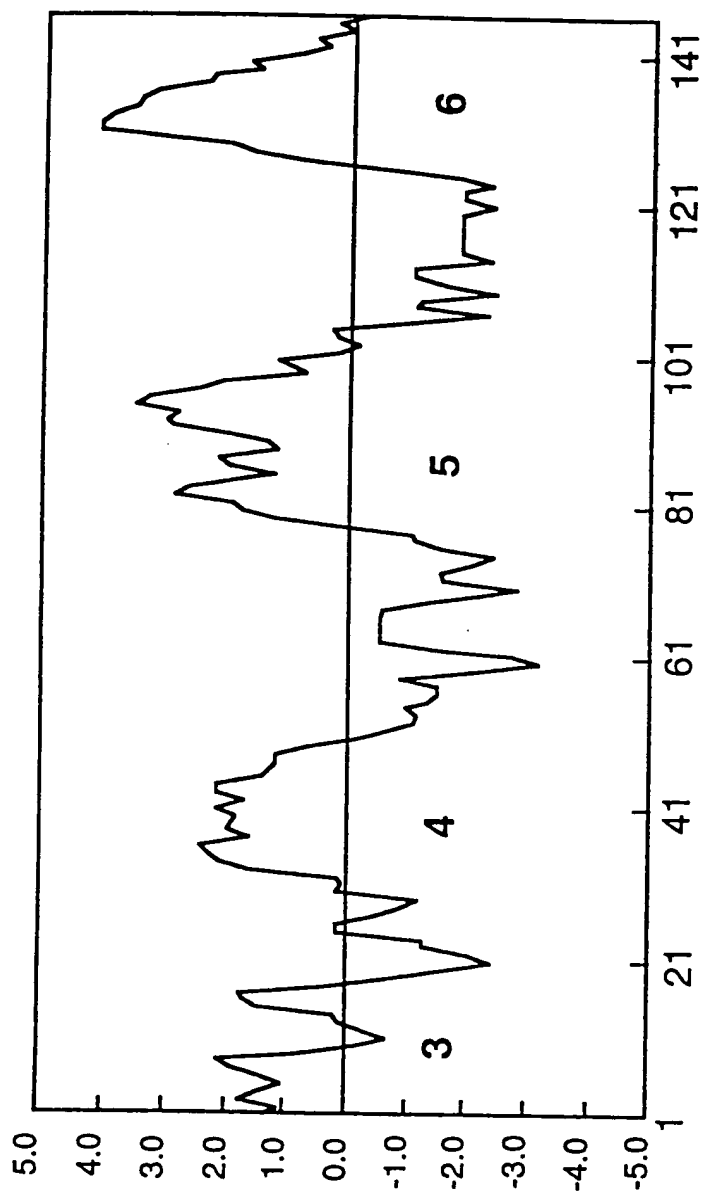
p3H2-17	1	VGLVGNILAS	10	WHKRGRRRA	20	WVVCGVVWLA	30	VTAQCLPTAV	40	FAATG IQRN-	50
p34996	1	RYTGAVHPLK		SLGRLKKNA		VYVSSLVWAL		VVAVIAPILF		YSGTGVRRN-	50
A46226	1	RYLAVVHPTR		SARWRITAPVA		RTVSAAVWVA		SAVVVLPPVV		E--SGVPRG-	50
JN0605	1	RYVAVVHPLR		AATYRRPSVA		KLINLGVWLA		SLLVTLPIAI		FADTRPARGG	50
S28787	1	RYLAI VHATN		SQKPRKLLAE		KVVYVGVWLP		AVLLTIPDLI		FADIKEVDE-	50
p3H2-17	51	RTV-CYDIL--	60	SPPILSTRYL	70	PYGMALTVIG	80	FLLPFIALLA	90	CYCRMARRLC	100
p34996	51	KITTCYDIT--		TADYLRSEF		VYSMCTIVFM		FCIPFIVILG		CYGLIVKALI	100
A46226	51	MST-CHMQWP		EPAAAWRIAGE		I IY--TAAALG		FFGPLLVIICL		CYLLIVVKVR	100
JN0605	51	QAVACNLQWP		HPAWSAVFVV		YTF----LGL		FLLPVLAIGL		CYLLIVGKVR	100
S28787	51	RYI-CDRF--		YPSDLWL VVF		QFQ--HIVVG		LLLPGIVILS		CYGIISKLIS	100
p3H2-17	101	RQDGPA-GPV	110	AQE-RRS--K	120	AARMVAVVAA	130	VFALCWLPLY	140	150
p34996	101	YKDLDN-SPL		----RR--K		SIYLVIIIVLT		VFAVSYLEPFH		150
A46226	101	SAGRRVWAPS		CQRRRRSERR		VTRMVAVVAA		LFVLCWMPFY		150
JN0605	101	AVALLRA---G		WQRRRRSEKK		ITRLVLMVVV		VFVLCWMPFY		150
S28787	101	HSKG-----		YQKR-----K		ALKTTVILIL		TFACWLPLY		150

5'	10			19			28			37			46			55		
	GTG	GGC	CTG	GTG	GGC	AAC	TTC	CTG	GCC	GCG	ATG	TCT	GTG	GAT	CGC	TAC	GTG	GCC
	Val	Gly	Leu	Val	Gly	Asn	Phe	Leu	Ala	Ala	Met	Ser	Val	Asp	Arg	Tyr	Val	Ala
	64			73			82			91			100			109		
	ATT	GTG	CAC	TGG	CGG	CGC	TCC	TCC	TCC	CTC	AGG	GTG	TCC	CGC	AAC	GCA	CTG	CTG
	Ile	Val	His	Ser	Arg	Arg	Ser	Ser	Ser	Leu	Arg	Val	Ser	Arg	Asn	Ala	Leu	Leu
	118			127			136			145			154			163		
	GGC	GTG	GGC	TTC	ATC	TGG	GCG	CTG	TCC	ATC	GCC	ATG	GCC	TGG	CCG	GTG	GCC	TAC
	Gly	Val	Gly	Phe	Ile	Trp	Ala	Leu	Ser	Ile	Ala	Met	Ala	Ser	Pro	Val	Ala	Tyr
	172			181			190			199			208			217		
	CAC	CAG	CGT	CTT	TTC	CAT	CGG	GAC	AGC	AAC	CAG	ACC	TTC	TGC	TGG	GAG	CAG	TGG
	His	Gln	Arg	Leu	Phe	His	Arg	Asp	Ser	Asn	Gln	Thr	Phe	Cys	Trp	Glu	Gln	Trp
	226			235			244			253			262			271		
	CCC	AAC	AAG	CTC	CAC	AAG	AAG	GCT	TAC	GTG	GTG	TGC	ACT	TTC	GTC	TTT	GGG	TAC
	Pro	Asn	Lys	Leu	His	Lys	Lys	Ala	Tyr	Val	Val	Cys	Thr	Phe	Val	Phe	Gly	Tyr
	280			289			298			307			316			325		
	CTT	CTG	CCC	TTA	CTG	CTC	ATC	TGC	TTT	TGC	TAT	GCC	AAG	GTC	CTT	AAT	CAT	CTG
	Leu	Leu	Pro	Leu	Leu	Leu	Ile	Cys	Phe	Cys	Tyr	Ala	Lys	Val	Leu	Asn	His	Leu
	334			343			352			361			370			379		
	CAT	AAA	AAG	CTG	AAA	AAC	ATG	TCA	AAA	AAG	TCT	GAA	GCA	TCC	AAG	AAA	AAG	ACT
	His	Lys	Lys	Leu	Lys	Asn	Met	Ser	Lys	Lys	Ser	Glu	Ala	Ser	Lys	Lys	Lys	Thr
	388			397			406			415			424			433		
	GCA	CAG	ACC	GTC	CTG	GTC	GTC	GTT	GTA	GTA	TTT	GCC	CTC	TGC	TGG	CTG	CCT	TTC
	Ala	Gln	Thr	Val	Leu	Val	Val	Val	Val	Val	Phe	Ala	Leu	Cys	Trp	Leu	Pro	Phe

TAC 3'

Tyr

FIGURE 41



	10	20	30	40	50
p3H2-34	1 VGLVGNFLAA	MSVDRYVALV	HSRRSSSLRV	SRNALGVGF	IVALLSLIAMAS
JN0605	1 METSVEGFLIV	LSVDRYVAIV	HPLEAATYRR	PSVAKLINLG	VWLA SHAYTL
B41795	1 QFTSFICFLIV	MSIDRYLAIV	HPITKSAKWR	PRIAKMIIMA	VWGVSLPAYIL
A39297	1 METSIYCLFIV	LSVDRYVAIV	HPITKAAAYRR	PITVAKVNLG	VWVLSLIVLIL
p3H2-34	51 PVA-YHQRLE	HRDSNQTFQW	EQMPNKLHK-	-KAYVVCTFV	FGYLLPLLLI
JN0605	51 PLATFADTRP	ARGGQAVACN	LQMPHPANS-	-AVFVAYATFL	LGFLLPVLAII
B41795	51 RIMLYAGLRS	NQWGRSS-CT	INWPESEGAW	YTGFLIYTFIL	LGFLVPLTIL
A39297	51 PLVVFESRTAA	NSDGINA-CN	MLMPEPAQRW	LVGFVLYTFEL	MGFLLPVGAII
p3H2-34	101 CFCY----AK	VLNHLHKLLK	NMSKKSEASK	KKTAQTVLAV	VAVFALCWLIF
JN0605	101 GLCYLLIAGK	MRAVALRAQW	QQRPRSE---	KKITRLVLMV	VAVFVLCWMP
B41795	101 CLQYLEIHLK	VKSSGIRVGS	SKRKKSE---	KKVTRMVSIV	VAVFIFCWLIF
A39297	101 CLCYVLLIATK	MRMVALKAGW	QQRKRSE---	RKITLVVMV	VAVFVICWME
p3H2-34	151 EV.....	160	170	180	190
JN0605	151 EV.....
B41795	151 EV.....
A39297	151 EV.....

FIGURE 43

5'	10	19	28	37	46	55
	GTG GGC ATG GTG GGC AAC GTC CTC GTG TTC TTC GGC TTC ATC AAG					
	Val Gly Met Val Gly Asn Val Leu Val Leu Trp Phe Phe Gly Phe Ser Ile Lys					
	64	73	82	91	100	109
	AGG ACC CCC TTC TOC TTC TAC TTC CTC CAC CTG GCC AGC GCC GGC GGC TAC					
	Arg Thr Pro Phe Ser Val Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr					
	118	127	136	145	154	163
	CTC TTC AGC AAG GGC GTG TTC TOC CTC CTG AAC GCC GGC TTC CTG GGC ACC					
	Leu Phe Ser Lys Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr					
	172	181	190	199	208	217
	TTC GCC CAC TAT GTG CGC AGC GTG GCC CGG GTG CTC GGC CTC GGC TTC GTG					
	Phe Ala His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val					
	226	235	244	253	262	
	GCG GGC GTG AGC CTC CTG CCG GCC GTG AGC ATG GAG CGC TGC GCG TCT G 3'					
	Ala Gly Val Ser Leu Leu Pro Ala Val Ser Met Glu Arg Cys Ala Ser					

FIGURE 44

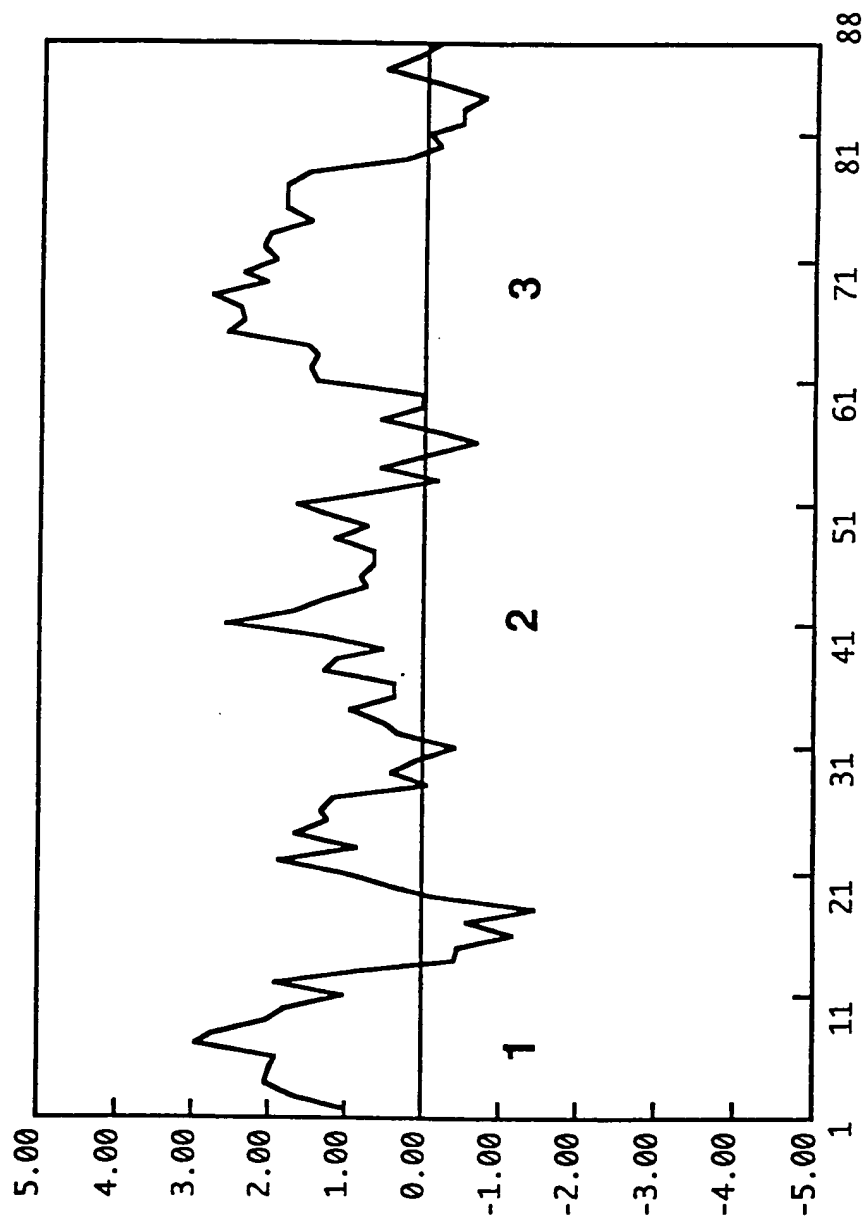


FIGURE 45

pMD4 A35639	10 1 VGMVGNVLVL 1 CGLVGNGLVL	20 WFFGFESIKRT WFFGFESIKRT	30 PFSVYRHLHA PFSIYRHLHA	40 SADGAYLFESK SADGIYLFESK	50 AVFSLLNACG AVIALLNMT	50 50
pMD4 A35639	60 51 FLGTFAHAYR 51 FLGSFPDYR	70 SVARVLGLCA RVSRIVGLCT	80 EVAGVSLLLPA FFAGVSLLLPA	90 VSMERCAAS ISIERCVS	100	100 100

FIGURE 46

1	CAAAGCAACAGGTGCAACCTCAAGGCACTGAAAGCAAGGGGACGCAGCTCACAAGGGCCAAGGGATTGAACC	72
1		1
73	CATAACCGCTCAGAAGATTCTCCGCCTGCGGAGAGCTGCGGAGGAGTCCCACCCGTCCAGCTTGCTGACTGC	144
1		1
145	GAGCAGTGAGAGTGGCTTAGACCGGTACCTCTGTGTTCTGGAGCCTGCCGCCCCGCACGGGAAAGGCTTAG	216
1		1
217	CTCGGCACTTGACAGACCGCTCTCTTTAGCCAGGCCAGGCACGAGGATAGTGTGATCGGGCACAGCCAGG	288
1		1
289	GTCGCTCTTCAGGCTTTCTTGCGGGTGGGGAGGTACTAGTTGGAGACGCGCGCTCGCTCTCGCCGCT	360
1		1
361	CTGCTCTGGGCCACTCCGTGATCCTAGGCTACCTCCAGAGCCAGTTTTCCCTGGCTGGCACAACCTCTCCAGG	432
1		1
433	GCGCTCCGGTCCGTTGCACAGCGCCCCAAGGGGTATCCAGTAAGTGATGGAACCTGGCTATGGTGAACCTC	504
1	MetGluLeuAlaMetValAsnLeu	8
505	AGTGAAGGGAATGGGAGCGACCCAGAGCCGCCAGCCCCGAGTCCAGGCCGCTCTTCGGCATTTGGCGTGGAG	576
8	SerGluGlyAsnGlySerAspProGluProProAlaProGluSerArgProLeuPheGlyIleGlyValGlu	32
577	AACTTCATTACGCTGGTAGTGTGTTGGCCTGATTTTCGGATGGGCGTCTGGGCAACAGCCTGGTGATCACC	648
32	AsnPheIleThrLeuValValPheGlyLeuIlePheAlaMetGlyValLeuGlyAsnSerLeuValIleThr	56
649	GTGCTGGCGCGCAGCAAACAGGCAAGCCGCGCAGCACCAACCTGTTTATCCTCAATCTGAGCATCGCA	720
56	ValLeuAlaArgSerLysProGlyLysProArgSerThrThrAsnLeuPheIleLeuAsnLeuSerIleAla	80
721	GACCTGGCTACCTGCTCTTCTGCATCCCTTTTCAGGCCACCGTGTATGCACTGCCACCTGGGTGCTGGGC	792
80	AspLeuAlaTyrLeuLeuPheCysIleProPheGlnAlaThrValTyrAlaLeuProThrTrpValLeuGly	104
793	GCCTTCATCTGCAAGTTTATACACTACTTCTTCACCGTGTCCATGCTGGTGAGCATCTTCACCTGGCCGCG	864
104	AlaPheIleCysLysPheIleHisTyrPhePheThrValSerMetLeuValSerIlePheThrLeuAlaAla	128
865	ATGCTGTGGATCGCTACGTGGCCATTGTGCACTCGCGCGCTCTCTCCCTCAGGTGTCCCGCAACGCA	936
128	MetSerValAspArgTyrValAlaIleValHisSerArgArgSerSerSerLeuArgValSerArgAsnAla	152
937	CTGCTGGGCGTGGGCTTCATCTGGGCGTGTCCATCGCCATGGCCTCGCCGGTGGCTACCACAGCGTCTT	1008
152	LeuLeuGlyValGlyPheIleTrpAlaLeuSerIleAlaMetAlaSerProValAlaTyrHisGlnArgLeu	176
1009	TTCCATCGGGACAGCAACCAGACCTTCTGCTGGGAGCAGTGGCCCAACAAGCTCCACAAGAAGGCTTACGTG	1080
176	PheHisArgAspSerAsnGlnThrPheCysTrpGluGlnTrpProAsnLysLeuHisLysLysAlaTyrVal	200
1081	GTGTGCACTTTTCGCTTTTGGGTACCTTCTGCCCTTACTGCTCATCTGCTTTTGCTATGCCAAGGTCCTTAAT	1152
200	ValCysThrPheValPheGlyTyrLeuLeuProLeuLeuLeuIleCysPheCysTyrAlaLysValLeuAsn	224
1153	CATCTGCATAAAAAGCTGAAAAACATGTCAAAAAGTCTGAAGCATCCAAGAAAAGACTGCACAGACCGTC	1224
224	HisLeuHisLysLysLeuLysAsnMetSerLysLysSerGluAlaSerLysLysLysThrAlaGlnThrVal	248
1225	CTGGTGGTCTGTTAGTATTGGCATATCCTGGCTGCCCCATCATGTGCTCCACCTCTGGGCTGAGTTTGGA	1296
248	LeuValValValValValPheGlyIleSerTrpLeuProHisHisValValHisLeuTrpAlaGluPheGly	272
1297	GCCTTCCCACTGACGCCAGCTTCTTCTTCTCAGAATCACCGCCCATTCCTGGCATAACGCAACTCCTCA	1368
272	AlaPheProLeuThrProAlaSerPhePheArgIleThrAlaHisCysLeuAlaTyrSerAsnSerSer	296
1369	GTGAACCCCATCATATATGCCTTTCTCTCAGAAAACCTCCGGAAGGCGTACAAGCAAGTGTTCAAGTGTCAT	1440
296	ValAsnProIleIleTyrAlaPheLeuSerGluAsnPheArgLysAlaTyrLysGlnValPheLysCysHis	320
1441	GTTTGGCATGAATCTCCACGCAGTGAAACTAAGGAAAACAAGAGCCGGATGGACACCCCGCCATCCACCAAC	1512
320	ValCysAspGluSerProArgSerGluThrLysGluAsnLysSerArgMetAspThrProProSerThrAsn	344
1513	TGCACCCACGTGTGAAGGTTTGCGGGAGCCTCCCGACTTCCAGCTCCCATGTGTGTTAGAGAGAGGAGGGCG	1584
344	CysThrHisVal***	349
1585	GAGCGAATTATCAAGTAACATGG	1607
349		349

FIGURE 47

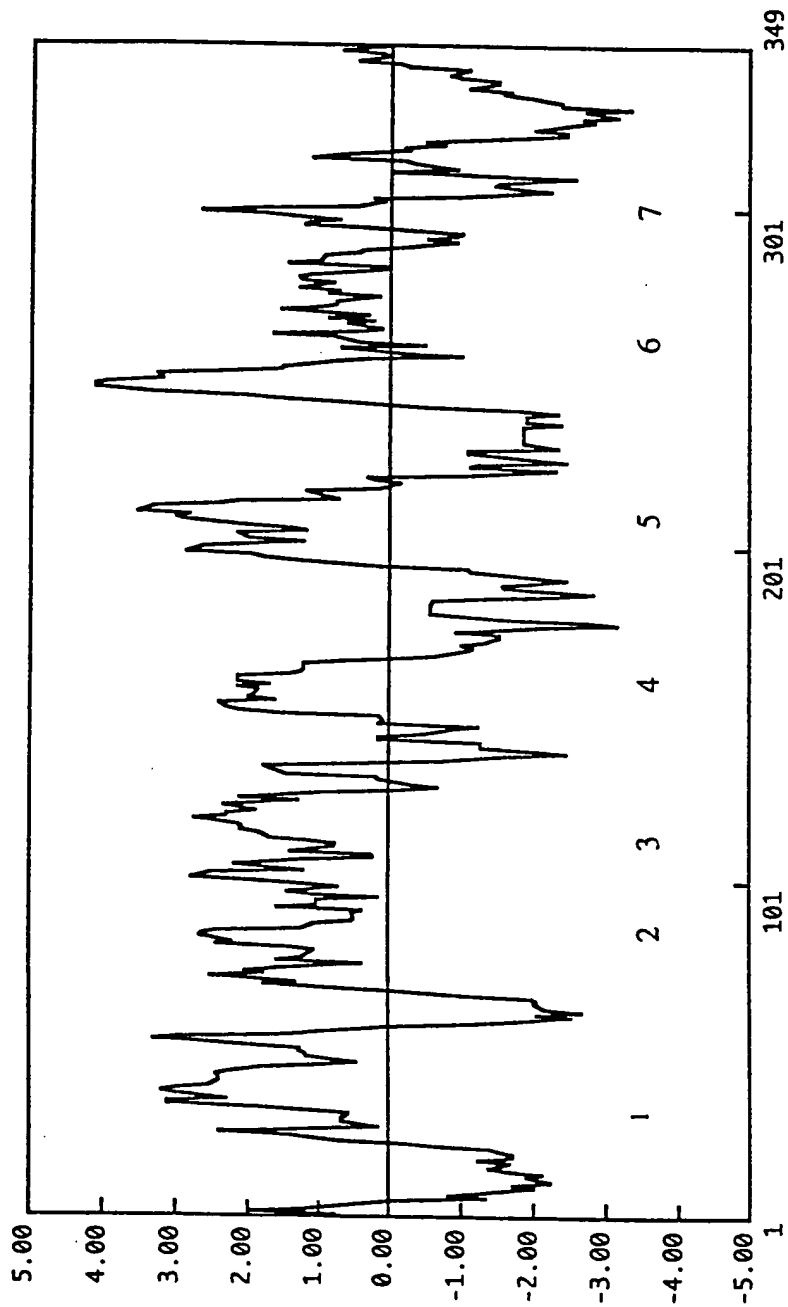


FIGURE 48

MOUSEGALRECE HUMGALAMI	1 1	10 10	20 20	30 30	40 40	50 50
		MELAVNLSSE MELAVNLSSE	GNASDPEPPA GNASDPEPPA	PEBRPLEGIG PEBRPLEGIG	VENFTTLAVF VENFTTLAVF	GLIFAVGVIG GLIFAVGVIG
MOUSEGALRECE HUMGALAMI	51 51	60 60	70 70	80 80	90 90	100 100
		NSLVITVLEAR NSLVITVLEAR	SKPCKPRSTT SKPCKPRSTT	NLFITNLSIA NLFITNLSIA	DIAYLLEFCIP DIAYLLEFCIP	EQATVVALPT EQATVVALPT
MOUSEGALRECE HUMGALAMI	101 101	110 110	120 120	130 130	140 140	150 150
		WLGAFICKF WLGAFICKF	IHYFFTVSML IHYFFTVSML	VSIFTLAAMS VSIFTLAAMS	VDRYVAIVHS VDRYVAIVHS	RRSSSLRVSR RRSSSLRVSR
MOUSEGALRECE HUMGALAMI	151 151	160 160	170 170	180 180	190 190	200 200
		NALLGVGFIW NALLGVGFIW	ALSIAMASPV ALSIAMASPV	AYHORLEH-R AYHORLEH-R	DSNOTFCWEQ DSNOTFCWEQ	WPKNLHKKAY WPKNLHKKAY
MOUSEGALRECE HUMGALAMI	201 201	210 210	220 220	230 230	240 240	250 250
		VCTFVFGYL VCTFVFGYL	LPLLLICFCY LPLLLICFCY	AKVLNHLHKK AKVLNHLHKK	LKMSKKSEA LKMSKKSEA	SKKTAQTIVL SKKTAQTIVL
MOUSEGALRECE HUMGALAMI	251 251	260 260	270 270	280 280	290 290	300 300
		VWVVFEGISM VWVVFEGISM	LPHHVHLMA LPHHVHLMA	EEGAFPLTPA EEGAFPLTPA	SFFFRITAHK SFFFRITAHK	LAYSNSVNP LAYSNSVNP
MOUSEGALRECE HUMGALAMI	301 301	310 310	320 320	330 330	340 340	350 350
		LIYAFLENEF LIYAFLENEF	RKAYKQVFKC RKAYKQVFKC	HVCDESPRSE HIRKDSLSD	TKENKSRMDT TKENKSRMDT	PPSTNCTHVK PPSTNCTHVK
MOUSEGALRECE HUMGALAMI	351 351	360 360	370 370	380 380	390 390	400 400
	
		X.....

FIGURE 49

5'	CTC	CGC	GCT	CTG	GGT	ATG	GAT	CGG	TAT	CTT	CTC	ACC	CTT	CAC	CCA	GTG	TGG	TCC
										Leu	Leu	Thr	Leu	His	Pro	Val	Trp	Ser
	CAA	AAG	CAC	CGA	ACC	TCA	CAC	TGG	GCT	TCC	AGA	GTC	GTT	CTG	GGA	GTC	TGG	CTC
	Gln	Lys	His	Arg	Thr	Ser	His	Trp	Ala	Ser	Arg	Val	Val	Leu	Gly	Val	Trp	Leu
	TCT	GCC	ACT	GCC	TTC	AGC	GTG	CCC	TAT	TTG	GTT	TTC	AGG	GAG	ACA	TAT	GAT	GAC
	Ser	Ala	Thr	Ala	Phe	Ser	Val	Pro	Tyr	Leu	Val	Phe	Arg	Glu	Thr	Tyr	Asp	Asp
	CGT	AAA	GGA	AGA	GTG	ACC	TGC	AGA	AAT	AAC	TAC	GCT	GTG	TCC	ACT	GAC	TGG	GAA
	Arg	Lys	Gly	Arg	Val	Thr	Cys	Arg	Asn	Asn	Tyr	Ala	Val	Ser	Thr	Asp	Trp	Glu
	AGC	AAA	GAG	ATG	CAA	ACA	GTA	AGA	CAA	TGG	ATT	CAT	GCC	ACC	TGT	TTC	ATC	AGC
	Ser	Lys	Glu	Met	Gln	Thr	Val	Arg	Gln	Trp	Ile	His	Ala	Thr	Cys	Phe	Ile	Ser
	CGC	TTC	ATA	CTG	GGC	TTC	CTT	CTG	CCT	TTC	TTA	GTC	ATT	GGC	TTT	TGT	TAT	GAA
	Arg	Phe	Ile	Leu	Gly	Phe	Leu	Leu	Pro	Phe	Leu	Val	Ile	Gly	Phe	Cys	Tyr	Glu
	AGA	GTA	GCC	CGC	AAG	ATG	AAA	GAG	AGG	GGC	CTC	TTT	AAA	TCC	AGC	AAA	CCC	TTC
	Arg	Val	Ala	Arg	Lys	Met	Lys	Glu	Arg	Gly	Leu	Phe	Lys	Ser	Ser	Lys	Pro	Phe
	AAA	GTC	ACG	ATG	ACT	GCT	GTT	ATC	TCT	TTT	TTC	TGT	CCT	GGC	TTC	CCT	ACC	ACA
	Lys	Val	Thr	Met	Thr	Ala	Val	Ile										

TG 3'

—

FIGURE 50

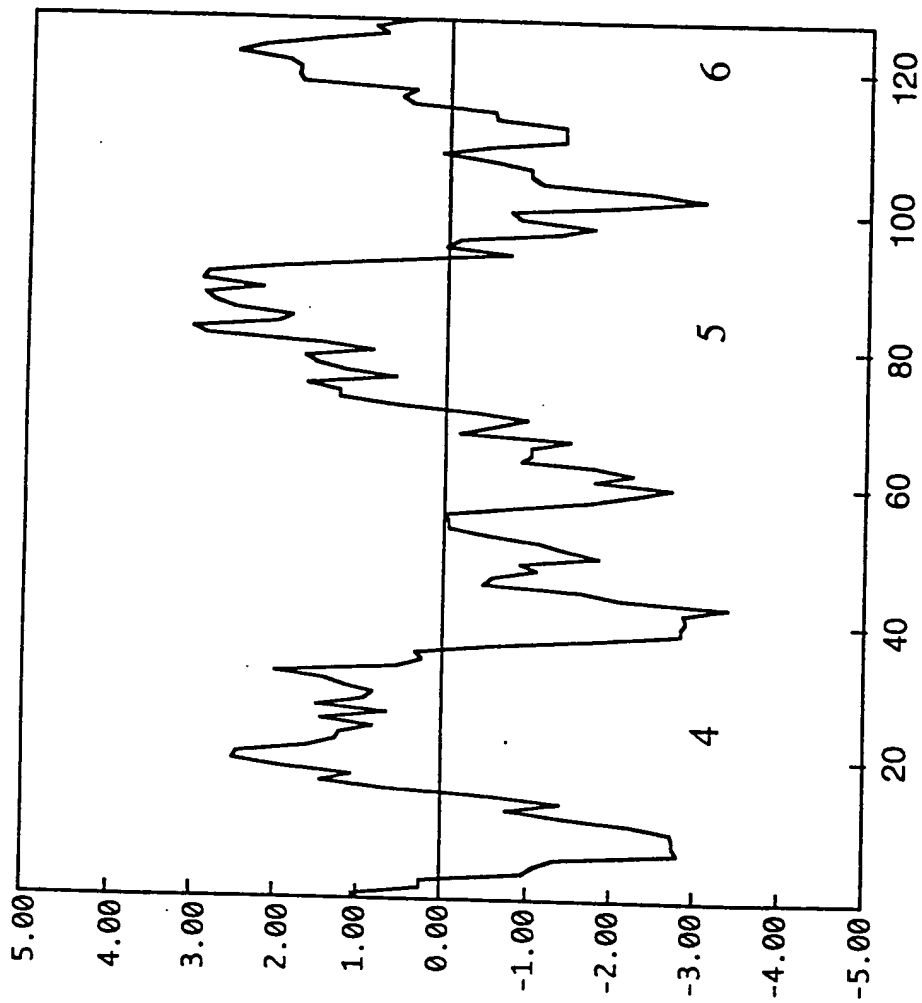


FIGURE 51

pmj10	1	10	20	30	40	50	
B42009	1	1	1	1	1	1	50
JC2014	1	1	1	1	1	1	50
A46520	1	1	1	1	1	1	50
A46525	1	1	1	1	1	1	50
S28787	1	1	1	1	1	1	50
pmj10	51	60	70	80	90	100	
B42009	51	51	51	51	51	51	100
JC2014	51	51	51	51	51	51	100
A46520	51	51	51	51	51	51	100
A46525	51	51	51	51	51	51	100
S28787	51	51	51	51	51	51	100
pmj10	101	110	120	130	140	150	
B42009	101	101	101	101	101	101	150
JC2014	101	101	101	101	101	101	150
A46520	101	101	101	101	101	101	150
A46525	101	101	101	101	101	101	150
S28787	101	101	101	101	101	101	150

FIGURE 52

5'	CTG	ACT	GCT	CTG	GGG	ACT	GAC	CGG	TAT	TTC	AAG	ATT	GTG	AAG	CCC	CTT	TCC	ACG	54
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
										Phe	Lys	Ile	Val	Lys	Pro	Leu	Ser	Thr	
	TCC	TTC	ATC	CAG	TCT	GTG	AAC	TAC	AGC	AAA	CTC	GTC	TCG	CTG	GTG	GTC	TGG	TTG	108
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Ser	Phe	Ile	Gln	Ser	Val	Asn	Tyr	Ser	Lys	Leu	Val	Ser	Leu	Val	Val	Trp	Leu	
	CTC	ATG	CTC	CTC	CTC	GCC	GTC	CCC	AAC	GTC	ATT	CTC	ACC	AAC	CAG	AGA	GTT	AAG	162
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Leu	Met	Leu	Leu	Leu	Ala	Val	Pro	Asn	Val	Ile	Leu	Thr	Asn	Gln	Arg	Val	Lys	
	GAC	GTG	ACG	CAG	ATA	AAA	TGC	ATG	GAA	CTT	AAA	AAC	GAA	CTG	GGC	CGC	CAG	TGG	216
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Asp	Val	Thr	Gln	Ile	Lys	Cys	Met	Glu	Leu	Lys	Asn	Glu	Leu	Gly	Arg	Gln	Trp	
	CAC	AAG	GCG	TCA	AAC	TAC	ATC	TTT	GTG	GGC	ATT	TTC	TGG	CTT	GTG	TTC	CTT	TTG	270
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	His	Lys	Ala	Ser	Asn	Tyr	Ile	Phe	Val	Gly	Ile	Phe	Trp	Leu	Val	Phe	Leu	Leu	
	CTA	ATC	ATT	TTC	TAC	ACT	GCT	ATC	ACC	AGG	AAA	ATC	TTT	AAG	TCC	CAC	CTG	AAA	324
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Leu	Ile	Ile	Phe	Tyr	Thr	Ala	Ile	Thr	Arg	Lys	Ile	Phe	Lys	Ser	His	Leu	Lys	
	TCC	AGA	AAG	AAT	TCC	ATC	TCG	GTC	AAA	AAG	AAA	TCT	AGC	CGC	AAC	ATC	TTC	AGC	378
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Ser	Arg	Lys	Asn	Ser	Ile	Ser	Val	Lys	Lys	Lys	Ser	Ser	Arg	Asn	Ile	Phe	Ser	
	ATC	GTG	TTT	ATC	CTC	TGT	TGG	CCC	CCC	TAC	CAC	ATC							3'
	---	---	---	---	---	---	---	---	---	---	---	---							
	Ile	Val																	

09036572-031198

FIGURE 53

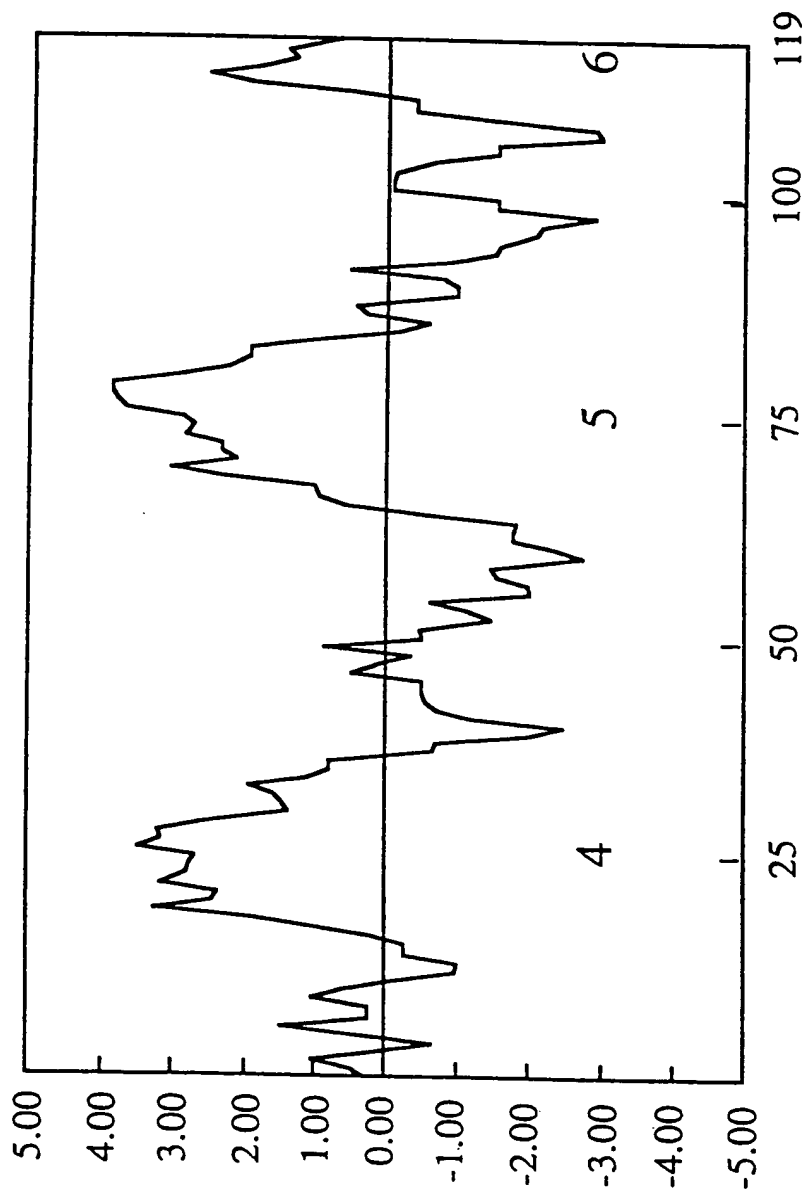


FIGURE 54

pmH28	1	FKIVKPLSTIS	10	FIQSVNYSKL	20	VSLVWLLML	30	LLAVPNMILT	40	NQRVKDVTQI	50
P35343	1	LAIVHATST-		LQKRHLVKF		VCIAMWLESV		IILALPILILR		NPVKVNLSTL	50
A41795	1	VAVVHPKAA		RYRRPTVAKV		VNLGYWVESL		LVI LPIVVS		RTAANSDCIV	50
A47457	1	VAVVHPLRAA		TYRRPSVAKL		INLGVWLASE		LVTETPIAIFA		DTRPARGGQ-	50
pmH28	51	KCME-LKNEI	60	GRQW HKASNY	70	IFVGIF-WLV	80	FLLIIFFYTA	90	IT-RKIFKSH	100
P35343	51	VCEVGVGNNT		SRL--RVWLR		ILPQTEGFLV		PFLIMLFCYG		FTLRITLFAH	100
A41795	51	ACNM-LMPEP		AQRWLVGEV-		LYTFELMGELL		PVGAICLCYW		LIIAKMRMVA	100
A47457	51	AVAC-NLQWP		HPAWSAVFEV-		VYTFELLCFLL		EVLAIGLCYL		LIVGKMRAVA	100
pmH28	101	LKSRKNSI-S	110	VKKKSSRNIF	120	S--IV	130	140	150
P35343	101	MG----QKHR		AMR----VIF		AVLV		150
A41795	101	EKAGWQQRKR		SERKTTLMVM		MVMV		150
A47457	101	LRAGWQQRKR		SEKKTITRLVL		MVMV		150

5 5 / 7 9

FIGURE 55

5' GCC ACC AAC GTG TTC ATC CTG TGT CTG GTG GAC CTG CTG GCT GCC CTG ACC CTC
 --- --- --- --- --- --- --- ---
 Val Asp Leu Leu Ala Ala Leu Thr Leu

63 72 81 90 99 108
 ATG CCT CTG GCC ATG CTC TCC AGC TCC GCC CTC TTT GAC CAC GCC CTC TTT GGG
 --- --- --- --- --- --- --- ---
 Met Pro Leu Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly

117 126 135 144 153 162
 GAG GTG GCC TGC CGC CTC TAC TTG TTC CTG AGC GTC TGC TTT GTC AGC CTG GCC
 --- --- --- --- --- --- --- ---
 Glu Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu Ala

171 180 189 198 207 216
 ATC CTC TCG GTG TCC GCC ATC AAT GTG GAG CGC TAC TAT TAT GTG GTC CAC CCC
 --- --- --- --- --- --- --- ---
 Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val Val His Pro

225 234 243 252 261 270
 ATG CGC TAT GAG GTG CGC ATG AAA CTG GGG CTG GTG GCC TCT GTG CTG GTG GGC
 --- --- --- --- --- --- --- ---
 Met Arg Tyr Glu Val Arg Met Lys Leu Gly Leu Val Ala Ser Val Leu Val Gly

279 288 297 306 315 324
 GTG TGG GTG AAG GCC CTG GCC ATG GCT TCT GTG CCA GTG TTG GGA AGG GTG TCC
 --- --- --- --- --- --- --- ---
 Val Trp Val Lys Ala Leu Ala Met Ala Ser Val Pro Val Leu Gly Arg Val Ser

333 342 351 360 369 378
 TGG GAG GAA GGC CCT CCC AGT GTC CCC CCA GGC TGT TCA CTC CAA TGG AGC CAC
 --- --- --- --- --- --- --- ---
 Trp Glu Glu Gly Pro Pro Ser Val Pro Pro Gly Cys Ser Leu Gln Trp Ser His

387 396 405 414 423 432
 AGT GCC TAC TGC CAG CTT TTC GTG GTG GTC TTC GCC GTC CTC TAC TTC CTG CTG
 --- --- --- --- --- --- --- ---
 Ser Ala Tyr Cys Gln Leu Phe Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu

441 450 459 468 477 486
 CCC CTG CTC CTC ATC CTT GTG GTC TAC TGC AGC ATG TTC CGG GTG GCT CGT GTG
 --- --- --- --- --- --- --- ---
 Pro Leu Leu Leu Ile Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val

495 504 513 522 531 540
 GCT GCC ATG CAG CAC GGG CCG CTG CCC ACG TGG ATG GAG ACG CCC CGG CAA CGC
 --- --- --- --- --- --- --- ---
 Ala Ala Met Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg

09033572-031199

FIGURE 56

549 558 567 576 585 594
 TCC GAG TCT CTC AGC AGC CGC TCC ACT ATG GTC ACC AGC TCG GGG GCC CCG CAG

 Ser Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro Gln

 603 612 621 630 639 648
 ACC ACC CCT CAC CGG ACG TTT GGC GGA GGG AAG GCA GCA GTG GTC CTC CTG GCT

 Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val Leu Leu Ala

 657 666 675 684 693 702
 GTG GGA GGA CAG TTC CTG CTC TGT TGG TTG CCC TAC TTC TCC TTC CAC CTC TAT

 Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe Ser Phe His Leu Tyr

 711 720 729 738 747 756
 GTG GCC CTG AGC GCT CAG CCC ATT GCA GCG GGG CAG GTG GAG AAC GTG GTG ACC

 Val Ala Leu Ser Ala Gln Pro Ile Ala Ala Gly Gln Val Glu Asn Val Val Thr

 765 774 783 792 801 810
 TGG ATT GGC TAC TTC TGC TTC ACC TCC AAC CCT CTC CTC TAT TCC TTC CTC CCT 3'

 Trp Ile Gly Tyr Phe Cys Phe Thr Ser

06030572.03198

FIGURE 57

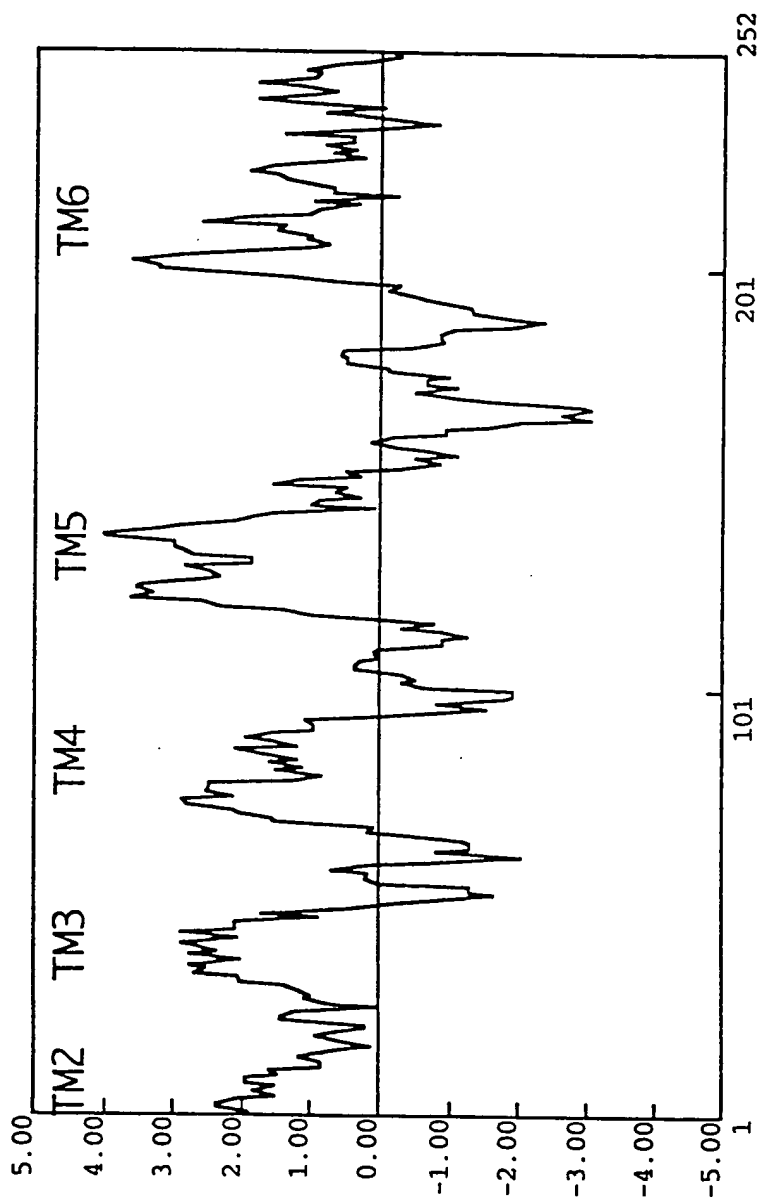


FIGURE 58

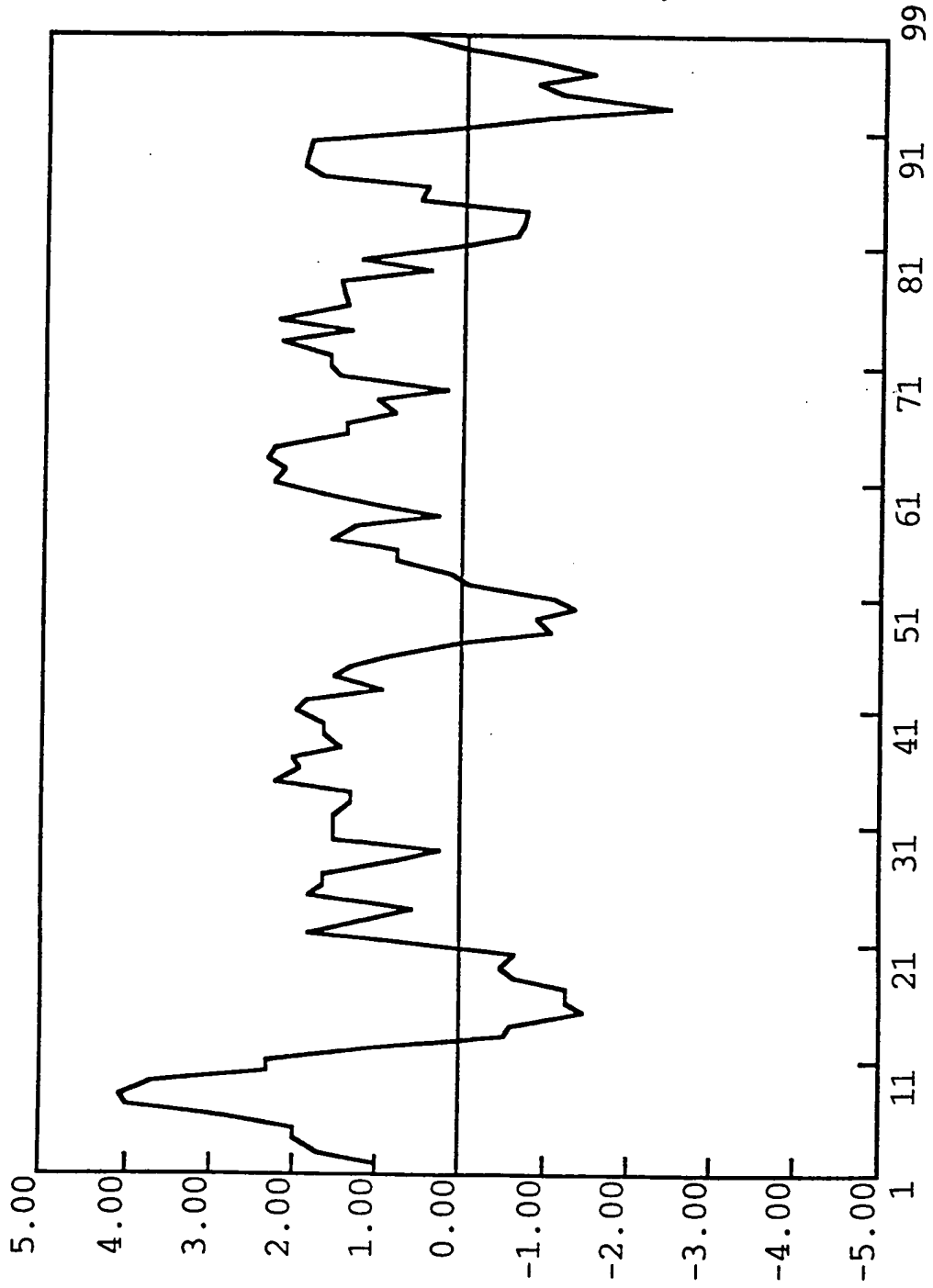


FIGURE 59

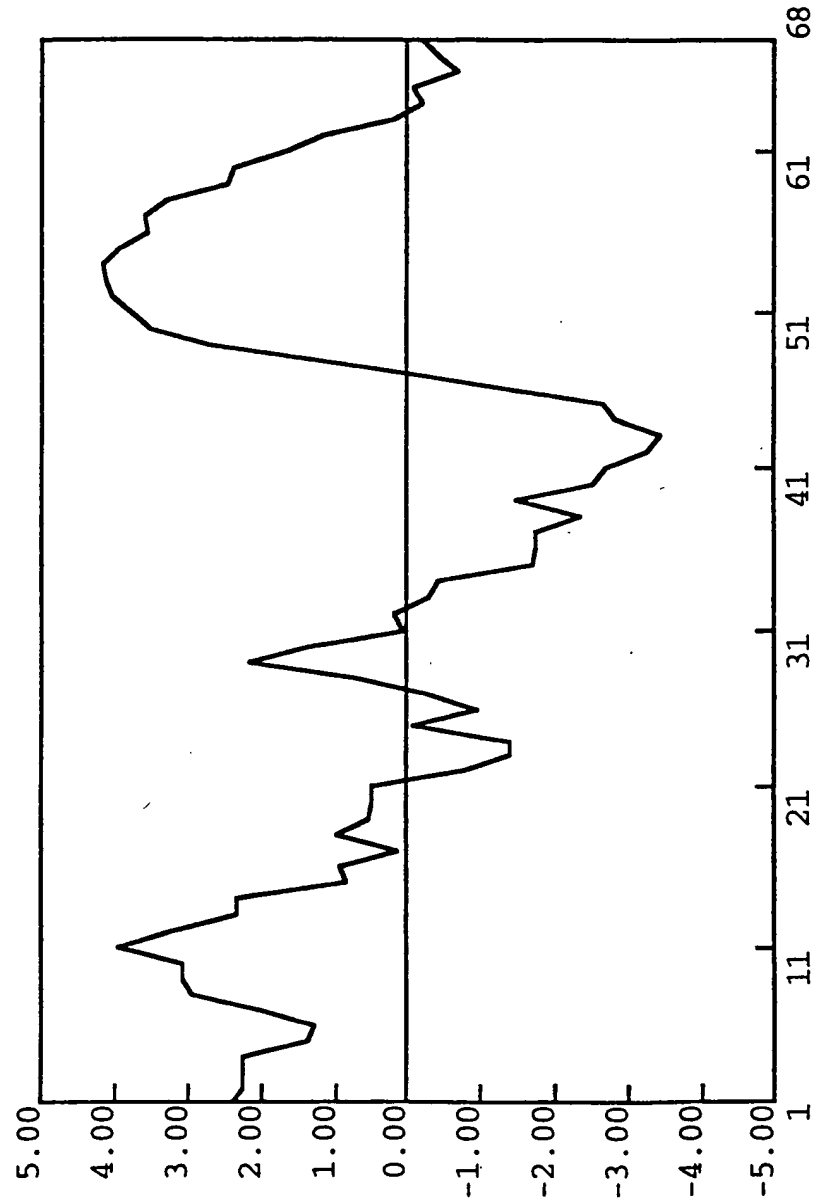


FIGURE 60

p19P2	10	20	30	40	50
S12863	1 VGMVGNVL LV	LV TARVRRLLH	NVTFNFIICNL	ALSDVLMCTA	CVPLTLAYAF
	1 LGVSGNLA EI	II ILKQKEMR	NVTFNFIICNL	SFSDLLEVAVM	CLPFITFVYTL
					50
p19P2	60	70	80	90	100
S12863	51 EPRGWVFGGG	LCHLVFLOP	VIVVVSVEFTL	TTIAVDRYVV	LVHPLRRRI-
	51 MDH-WVFGET	MCKLNPEVQC	VSITVSIIESL	VLIAVERHQL	IINPRGWRPN
					100
p19P2	110	120	130	140	150
S12863	101 -----	-----	-----	-----	-----
	101 NRHAYIGITV	IWVLAVASSL	PFVIYQILTD	EPFQNVSLAA	FKDKYVCFDK
					150
p19P2	160	170	180	190	200
S12863	151 -----GLLV	TVLPLLVIL	LS-----	VRVSVKLRNR	VVPGCVTQSQ
	151 FPSDSHR LSY	TTLLLVLEQYF	GPLCFIFICY	FKIYIREKR	NNMMDKIRDS
					200
p19P2	210	220	230	240	250
S12863	201 ADWDRARRRR	TFCLLAVVAVV	VFATCWLPPY
	201 KYRSSETKRI	NVMFLSI VVA	-EAVCWLPLT
					250

	1	10	20	30	40	50
p19P2	1	VGMVGNVLLV	LVIARVRRLH	NVTENFLIGNL	ALSDVLMCTA	CVPLTLAYAF
PG3-2/pG1-10	1	VGMVGNITLV	LVIARVRRLY	NVTENFLIGNL	ALSDVLMCTA	CVPLTLAYAF
p19P2	51	EPRGMVFECCG	LCHLVFFLOP	VTVVSVSFTL	TTTAVDRVVV	LVHPLRRRI
PG3-2/pG1-10	51	EPRGMVFECCG	ECHLVFFELQA	VTVVSVSFTL	TTTAVDRVVV	LTVHPLRRRIS
p19P2	101	---	---	---	---	---
PG3-2/pG1-10	101	LRLSAYAVLA	IWVLSAVLAL	PAAVHTYHVE	LKPHDVRICE	EFWGSQERQR
p19P2	151	---	---	---	---	---
PG3-2/pG1-10	151	QLYAWGLLTV	TALLPLLVIL	LSYVRVSVKL	RNRVVPGCVT	QSQADWDRAR
p19P2	201	RRRTFCLLVV	VAVVFAICWL	PYY	---	---
PG3-2/pG1-10	201	RRRTFCLLVV	VAVVFTLCWL	PFF	---	---

FIGURE 62

5'	CTG	TGT	9	ATC	GCG	18	GTG	GAT	AGG	27	TAC	GTG	GTT	36	CTG	GTG	CAC	45	CCG	CTA	CGT	54	CGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Arg	Arg	Arg	Arg
	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63
	CGC	ATT	TCA	CTG	AGG	CTC	AGC	GCC	TAC	GCG	GTG	CTG	GGC	ATC	TGG	GCT	CTA	TCT	TCT	TCT	TCT	TCT	TCT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser	Ser	Ser	Ser	Ser	Ser
	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117
	GCA	GTG	CTG	GCG	CTG	CCG	GCC	GCG	GTG	CAC	ACC	TAC	CAT	GTG	GAG	CTC	AAG	CCC	CCC	CCC	CCC	CCC	CCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	Pro	Pro	Pro	Pro	Pro
	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171
	CAC	GAC	GTG	AGC	CTC	TGC	GAG	GAG	TTC	TGG	GGC	TGC	CAG	GAG	CGC	CAA	CGC	CAG	CAG	CAG	CAG	CAG	CAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	His	Asp	Val	Ser	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Arg	Gln	Arg	Gln	Arg
	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225
	ATC	TAC	GCC	TGG	GGG	CTG	CTT	CTG	GGC	ACC	TAT	TTC	CTC	CCC	CTG	CTG	GCC	ATC	ATC	ATC	ATC	ATC	ATC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	Ile	Ile	Ile	Ile	Ile	Ile
	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279
	CTC	CTG	TCT	TAC	GTA	CGG	GTG	TCA	GTG	AAG	CTG	AGG	AAC	CGC	GTG	GTG	CCT	GGC	GGC	GGC	GGC	GGC	GGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly	Gly	Gly	Gly	Gly	Gly
	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333
	AGC	GTG	ACC	CAG	AGT	CAA	GCT	GAC	TGG	GAC	CGA	GCG	CGT	CGC	CGC	CGC	ACT	TTC	TTC	TTC	TTC	TTC	TTC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe	Phe	Phe	Phe	Phe	Phe
	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387
	TGT	CTG	CTG	GTG	GTG	GTG	GTG	GTA	GTG	TTC	ACG	CTC	TGC	TGG	CTG	CCC	TTC	TAC	TAC	TAC	TAC	TAC	TAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr

CT 3'

--

--

09038572.03198

FIGURE 63

p19P2	1	10	20	30	40	50	
PG3-2/PG1-10	1	VGMVGNVLLV	LVIARVRRRH	NVTFNFIIGNL	ALSDVLMCTA	CVPLTLAYAF	50
p5S38	-79	VGMVGNVLLV	LVFARVRRLV	NVTFNFIIGNL	ALSDVLMCTA	CVPLTLAYAF	50
							-30
p19P2	51	60	70	80	90	100	
PG3-2/PG1-10	51	EPRGMVFGGG	ECHLVFELOP	VTVVSVFETL	TTTAVDRVAV	LVHPLRRRI	100
p5S38	-29	EPRGMVFGGG	ECHLVFELOP	VTVVSVFETL	TTTAVDRVAV	LVHPLRRRI	100
					CVTAVDRVAV	LVHPLRRRI	21
p19P2	101	110	120	130	140	150	
PG3-2/PG1-10	101	LRLSAYAVLA	IMVLSAVLEAL	PAAVHTYHVE	LKPHDVR LCE	EFMGSQERQR	150
p5S38	22	LRLSAYAVLG	IMVLSAVLEAL	PAAVHTYHVE	LKPHDVS LCE	EFMGSQERQR	150
							71
p19P2	151	160	170	180	190	200	
PG3-2/PG1-10	151	GLLLV	TVLLPLLVIL	LSYVRVSVKL	RNRVVPGRVT	QSQADMDRAR	200
p5S38	72	QLYANGLLLV	TVLLPLLVIL	LSYVRVSVKL	RNRVVPGRVT	QSQADMDRAR	200
		QLYANGLLLG	TVLLPLLVIL	LSYVRVSVKL	RNRVVPGRVT	QSQADMDRAR	121
p19P2	201	210	220	230	240	250	
PG3-2/PG1-10	201	RRRTFCLLVV	VVVFALCWL	PVY			250
p5S38	122	RRRTFCLLVV	VVVFALCWL	PFE			250
				PFY			171

FIGURE 64

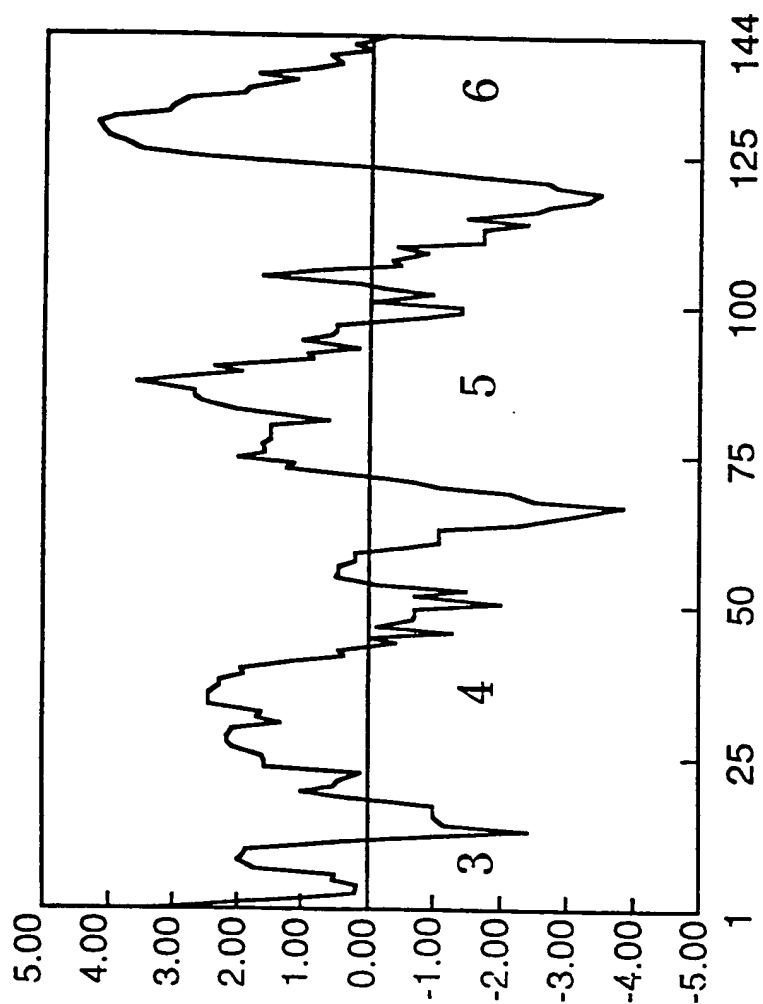


FIGURE 65

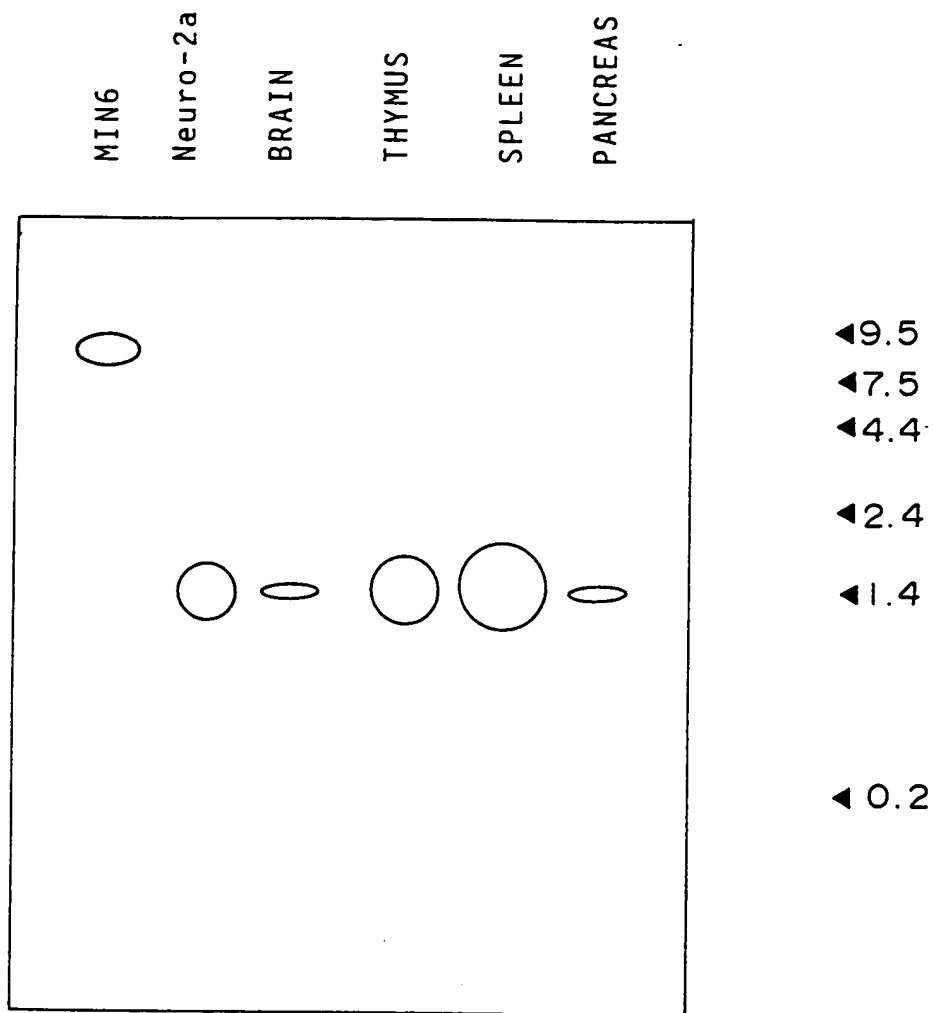
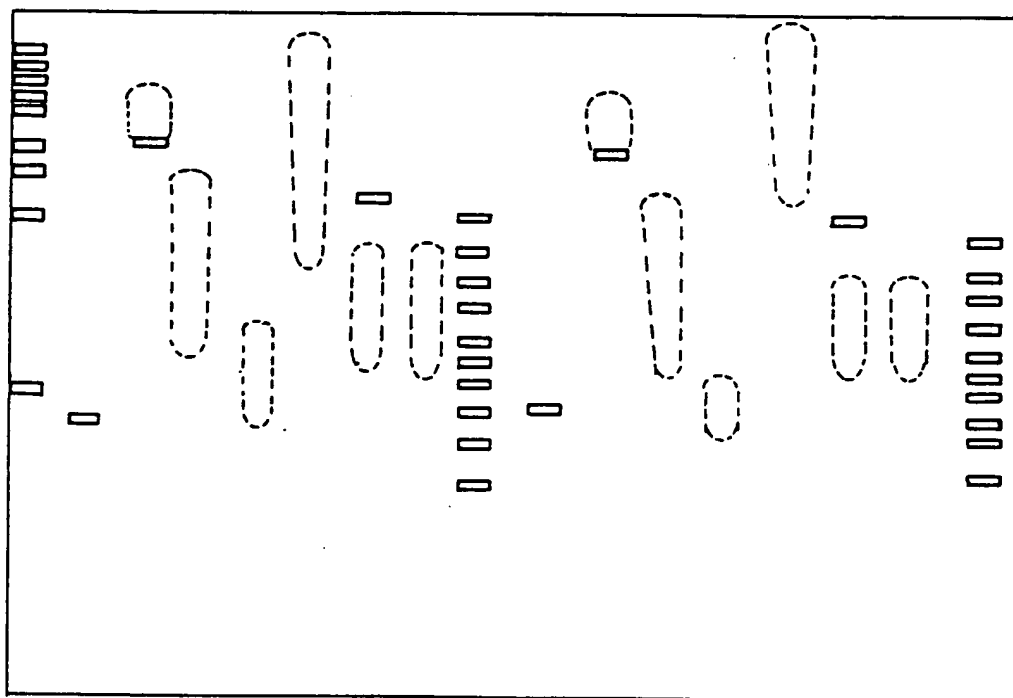


FIGURE 66

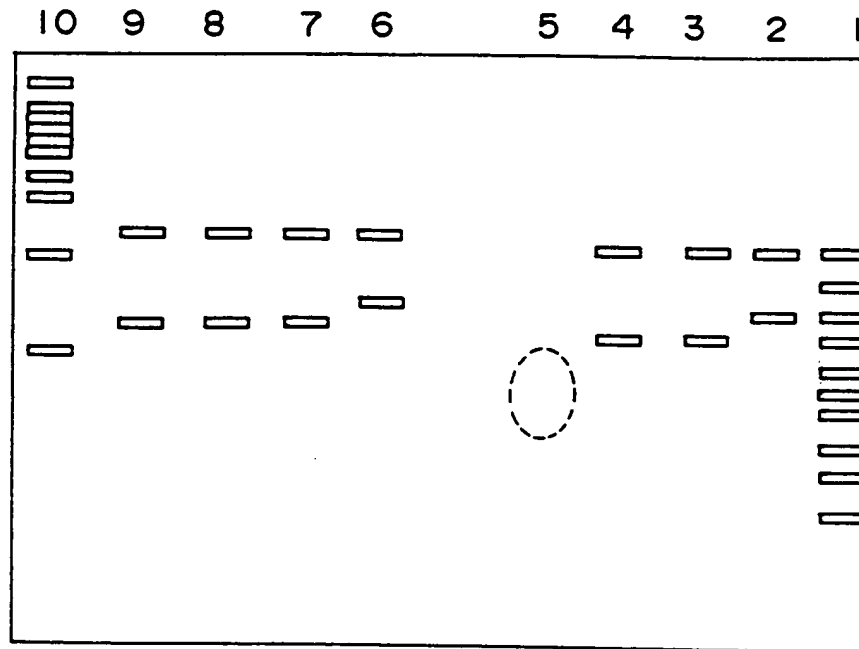
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17



86TTE0 2453E060

6 7 / 7 9

FIGURE 67



09038572-034498

FIGURE 68

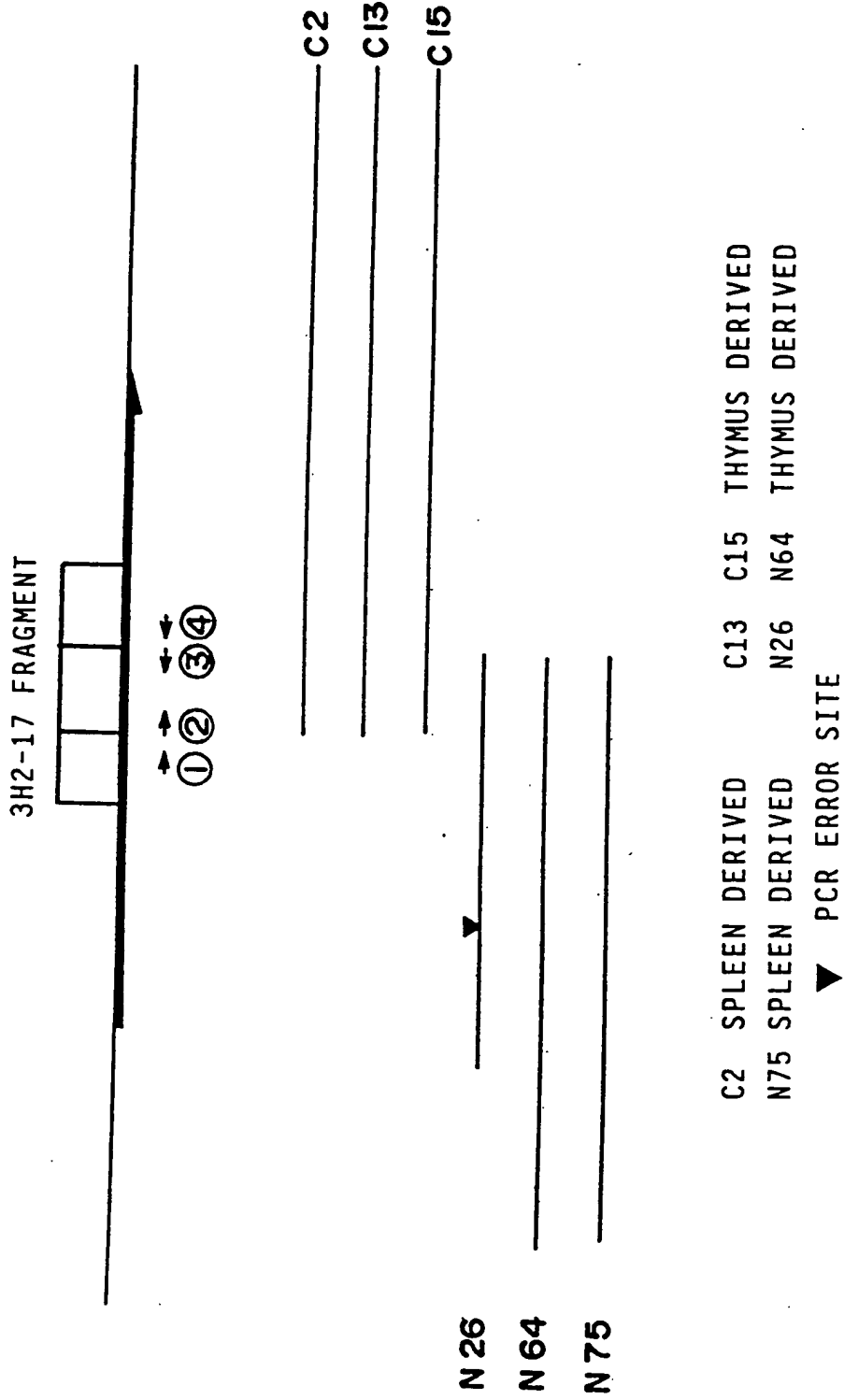


FIGURE 69

1	GAGCATAGGAAAGGCTGACAGGCAGTTATGGAGCAGGACAATGGCACCATCCAGGCTCCA	60
1	MetGluGlnAspAsnGlyThrIleGlnAlaPro	11
61	GGCTTGCCCGCCACACCTGCGTCTACCGTGAGGATTTCAAGCGACTGCTGCTAACCCCG	120
11	GlyLeuProProThrThrCysValTyrArgGluAspPheLysArgLeuLeuLeuThrPro	31
121	GTATACTCGGTGGTGGTGGTGGTGGCTGCCACTGAACATCTGCGTCATTGCCCCAGATC	180
31	ValTyrSerValValLeuValValGlyLeuProLeuAsnIleCysValIleAlaGlnIle	51
181	TGCGCATCCCGCGGACCTGACCCGTTCCGCTGTGTACACCCTGAACCTGGCACTGGCG	240
51	CysAlaSerArgArgThrLeuThrArgSerAlaValTyrThrLeuAsnLeuAlaLeuAla	71
241	GACCTGATGTATGCCTGTTCACCTACCCCTACTTATCTATAACTACGCCAGAGGGGACCAC	300
71	AspLeuMetTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaArgGlyAspHis	91
301	TGGCCCTTCGGAGACCTGGCCTGCCGCTTTGTACGCTTCCTCTCTATGCCAATCTACAT	360
91	TrpProPheGlyAspLeuAlaCysArgPheValArgPheLeuPheTyrAlaAsnLeuHis	111
361	GGCAGCATCCTGTCTCTCACCTGCATTAGCTTCCAGCGCTACCTGGGCATCTGCCACCCC	420
111	GlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIleCysHisPro	131
421	CTGGCTTCCTGGCACAAGCGTGGAGGTGCGCGTGCTGCTGGGTAGTGTGTGGAGTCGTG	480
131	LeuAlaSerTrpHisLysArgGlyGlyArgArgAlaAlaTrpValValCysGlyValVal	151
481	TGGCTGGCTGTGACAGCCAGTGCCTGCCCCAGGCAGTCTTTGCTGCCACAGGCATCCAG	540
151	TrpLeuAlaValThrAlaGlnCysLeuProThrAlaValPheAlaAlaThrGlyIleGln	171
541	CGCAACCGCACTGTGTGCTACGACCTGAGCCACCCATCCTGTCTACTCGCTACCTGCCC	600
171	ArgAsnArgThrValCysTyrAspLeuSerProProIleLeuSerThrArgTyrLeuPro	191
601	TATGGTATGGCCCTCACGGTCATCGGCTTCTTGCTGCCCTTCATAGCCTTACTGGCTTGT	660
191	TyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheIleAlaLeuLeuAlaCys	211
661	TATTGTGCAATGGCCCGCGCCTGTGTGCCAGGATGGCCCAGCAGGTCTGTGGCCCAA	720
211	TyrCysArgMetAlaArgArgLeuCysArgGlnAspGlyProAlaGlyProValAlaGln	231
721	GAGCGGCGCAGCAAGCGGGCTCGTATGGCTGTGGTGGTGGCAGCTGTCTTTGCCATCAGC	780
231	GluArgArgSerLysAlaAlaArgMetAlaValValAlaAlaValPheAlaIleSer	251
781	TTCCTGCCTTTCCACATCACCAAGACAGCCTACTTGGCTGTGCGCTCCACGCCCCGTGTC	840
251	PheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValArgSerThrProGlyVal	271
841	TCTTGCCCTGTGCTGGAGACCTTCGCTGCTGCCTACAAAGGCACTCGGCCCTTCGCCAGT	900
271	SerCysProValLeuGluThrPheAlaAlaAlaTyrLysGlyThrArgProPheAlaSer	291
901	GTCAACAGTGTCTTGACCCCATCTCTTCTACTTCACACAACAGAAGTTCGGCGGCAA	960
291	ValAsnSerValLeuAspProIleLeuPheTyrPheThrGlnGlnLysPheArgArgGln	311
961	CCCCACGATCTCTTACAGAGGCTCACAGCCAAGTGGCAGAGGCAGAGAGTCTGAGGCCCC	1020
311	ProHisAspLeuLeuGlnArgLeuThrAlaLysTrpGlnArgGlnArgVal***	329

09038572-03198

FIGURE 70

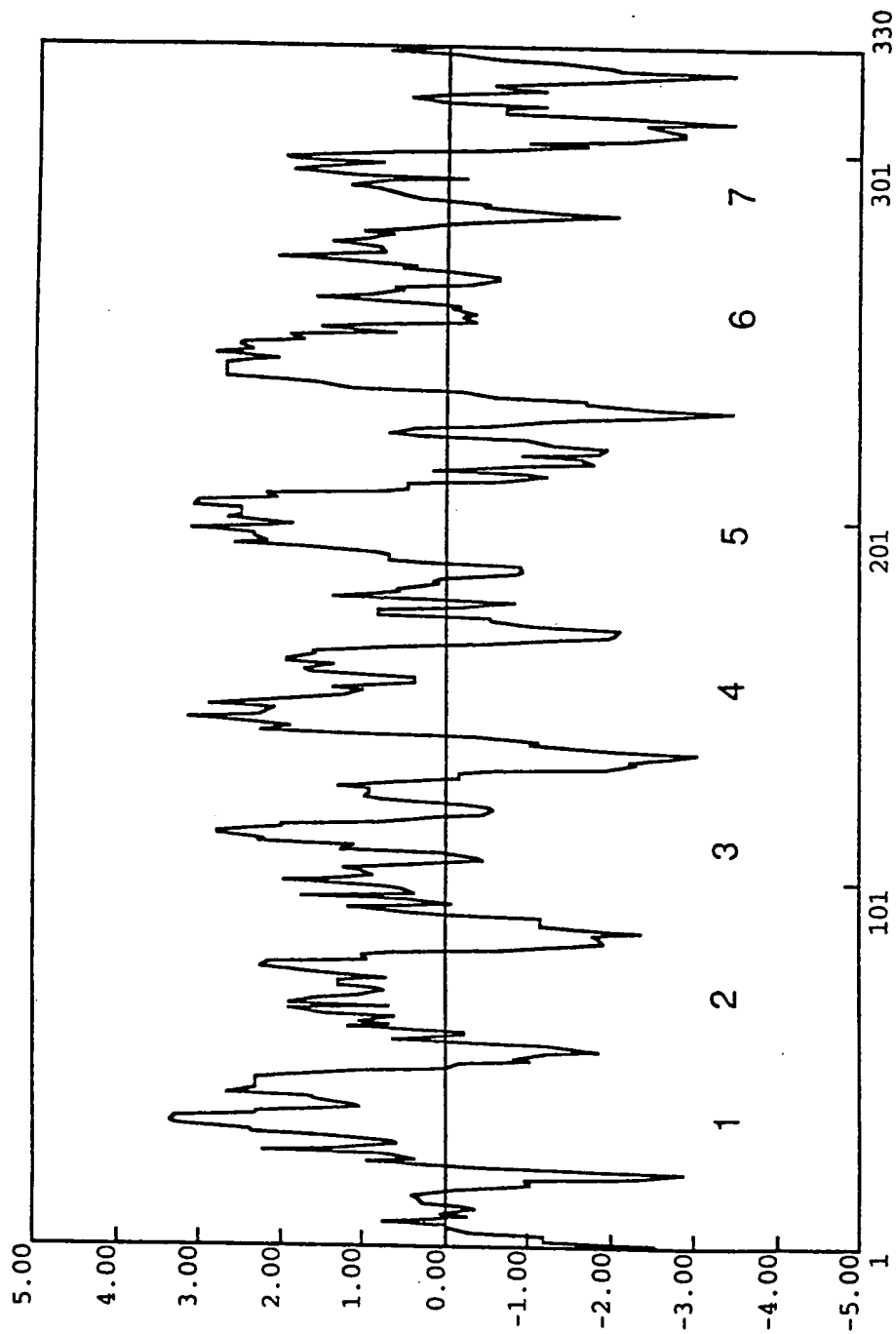


FIGURE 71

75+13, CODING	1	10	20	30	40	50	
P2UR_MOUSE	1	MAADLEPWNS	TINGIWEQDE	LGY-----	---KCRFN-E	DEKAVLL-P	50
P2YR_CHICK	1	ATEALISAAL	--NGI-S-PE	LAGGWAAGN	ATTKCSLTKT	GEQFYLL-ET	50
75+13, CODING	51	60	70	80	90	100	
P2UR_MOUSE	51	VSYGVVCLV	-LLENVVALY	-HFG-RLKI	ANA-SITVMF	HLAUSDSTVA	100
P2YR_CHICK	51	V-YILLVFTTS	FLG-NSVALW	M-E-VFHMSP	NSGIS-VYMF	NLAALADFLYV	100
75+13, CODING	101	110	120	130	140	150	
P2UR_MOUSE	101	ASLPPLLIVYV	ARG-DHNWPE	TLCKLVREF	FYVAILYCSIL	FLTCISVHRC	150
P2YR_CHICK	101	LTLPLALIVYV	FNKTP-RISG	DVMCKLORFI	SAVALYCSIL	FLTCISVHRY	150
75+13, CODING	151	160	170	180	190	200	
P2UR_MOUSE	151	LGICHPLASV	HKSGEE-EAA	WVVGCVVRLA	VTAOCL-EIA	VFAA-IGIOR	200
P2YR_CHICK	151	EGVLRPLHSI	--SAGRAVA	RRVAADVWVL	VLA-COAPVL	YFVT-TSVRG	200
	151	TSWVEPLKSL	G-SLKKN-A	VYVSSLVVAL	VWAVIA-EIL	-FVSGIGVRR	200
75+13, CODING	201	210	220	230	240	250	
P2UR_MOUSE	201	TR-ITCHDTS	ARE-LFSHEV	A-YSSVMLGL	LEAVEFSVIL	VGVLMARRL	250
P2YR_CHICK	201	NKMTTCYDIT	ADSYRSSEV	--YSHCTIVF	MCCI-PPIVIL	GVGLIVKAL	250
75+13, CODING	251	260	270	280	290	300	
P2UR_MOUSE	251	CRODGPAG-GE	VAQERRSKAA	--FMVVVAA	VEATSELPFH	IINKTAYLAVR	300
P2YR_CHICK	251	-LN--PAYGE	TGSLPFAARK	SVETALVLA	VEALCELPFH	VIRILAYSPR	300
	251	IYKD-LDENSE	---L-ERK--	SIYLVIIILT	VEAVSYLPFH	VMAILNLRAR	300
75+13, CODING	301	310	320	330	340	350	
P2UR_MOUSE	301	STP---GVSC	PVLETFAAAY	KCTREFASVN	SVLDPILEYF	TOKKERRPH	350
P2YR_CHICK	301	SID----LSC	HTLNAINMAY	KITRPLEASAN	SCIDPILVEL	AGORLVRFAR	350
	301	-LDFQTPQMC	AFNDKVYATV	QVTRGLASLN	SCVDPILVEL	AGDTERRRLS	350
75+13, CODING	351	360	370	380	390	400	
P2UR_MOUSE	351	ELLQRLTAKW	QRQRV*....	400
P2YR_CHICK	351	DAKPPTPTPT	SPQARRKGL	HRPNRTVRKD	LSVSSDDSR	TESTPAGSET	400
	351	RATRKSRRS	EPNVQSKSEE	MILNLTTEYK	QNGDTSL...	400
75+13, CODING	401	410	420	430	440	450	
P2UR_MOUSE	401	KDIRL.....	450
P2YR_CHICK	401	450

05036572.031198

FIGURE 72

5'	9			18			27			36			45			54		
	GCC	ACC	AAC	GTG	TTC	ATC	CTG	TCA	CTG	GCC	GAT	GTG	CTG	GTG	ACA	GCC	ATC	TGC
										Ala			Asp			Val		
										Leu			Val			Thr		
										Ala			Ile			Cys		
	63			72			81			90			99			108		
	CTG	CCG	GCC	AGT	CTG	CTG	GTA	GAC	ATC	ACG	GAA	TCC	TGG	CTC	TTT	GGC	CAT	GCC
	Leu	Pro	Ala	Ser	Leu	Leu	Val	Asp	Ile	Thr	Glu	Ser	Trp	Leu	Phe	Gly	His	Ala
	117			126			135			144			153			162		
	CTC	TGC	AAG	GTC	ATC	CCC	TAT	CTA	CAG	GCC	GTG	TCC	GTG	TCA	GTG	GTC	GTG	CTG
	Leu	Cys	Lys	Val	Ile	Pro	Tyr	Leu	Gln	Ala	Val	Ser	Val	Ser	Val	Val	Val	Leu
	171			180			189			198			207			216		
	ACT	CTC	AGC	TCC	ATC	GCC	CTG	GAC	CGC	TGG	TAC	GCC	ATC	TGC	CAC	CCG	CTG	TTG
	Thr	Leu	Ser	Ser	Ile	Ala	Leu	Asp	Arg	Trp	Tyr	Ala	Ile	Cys	His	Pro	Leu	Leu
	225			234			243			252			261			270		
	TTC	AAG	AGC	ACT	GCC	CGG	CGC	GCC	CGC	GGC	TCC	ATC	CTC	GGC	ATC	TGG	GCG	GTG
	Phe	Lys	Ser	Thr	Ala	Arg	Arg	Ala	Arg	Gly	Ser	Ile	Leu	Gly	Ile	Trp	Ala	Val
	279			288			297			306			315			324		
	TCG	CTG	GCT	GTC	ATG	GTG	CCT	CAG	GCT	GCT	GTC	ATG	GAG	TGT	AGC	AGC	GTG	CTG
	Ser	Leu	Ala	Val	Met	Val	Pro	Gln	Ala	Ala	Val	Met	Glu	Cys	Ser	Ser	Val	Leu
	333			342			351			360			369			378		
	CCC	GAG	CTG	GCC	AAC	CGC	ACC	CGC	CTC	CTG	TCT	GTC	TGT	GAT	GAG	CGC	TGG	GCA
	Pro	Glu	Leu	Ala	Asn	Arg	Thr	Arg	Leu	Leu	Ser	Val	Cys	Asp	Glu	Arg	Trp	Ala
	387			396			405			414			423			432		
	GAC	GAC	CTG	TAC	CCC	AAG	ATC	TAC	CAC	AGC	TGC	TTC	TTC	ATT	GTC	ACC	TAC	CTG
	Asp	Asp	Leu	Tyr	Pro	Lys	Ile	Tyr	His	Ser	Cys	Phe	Phe	Ile	Val	Thr	Tyr	Leu
	441			450			459			468			477			486		
	GCC	CCA	CTG	GGC	CTC	ATG	GCC	ATG	GCC	TAT	TTC	CAG	ATC	TTC	CGC	AAG	CTC	TGG
	Ala	Pro	Leu	Gly	Leu	Met	Ala	Met	Ala	Tyr	Phe	Gln	Ile	Phe	Arg	Lys	Leu	Trp
	495			504			513			522			531			540		
	GGC	CGC	CAG	ATC	CCC	GGC	ACC	ACC	TCG	GCC	CTG	GTG	CGC	AAC	TGG	AAG	CGG	CCC

BBT-2258E060

FIGURE 73

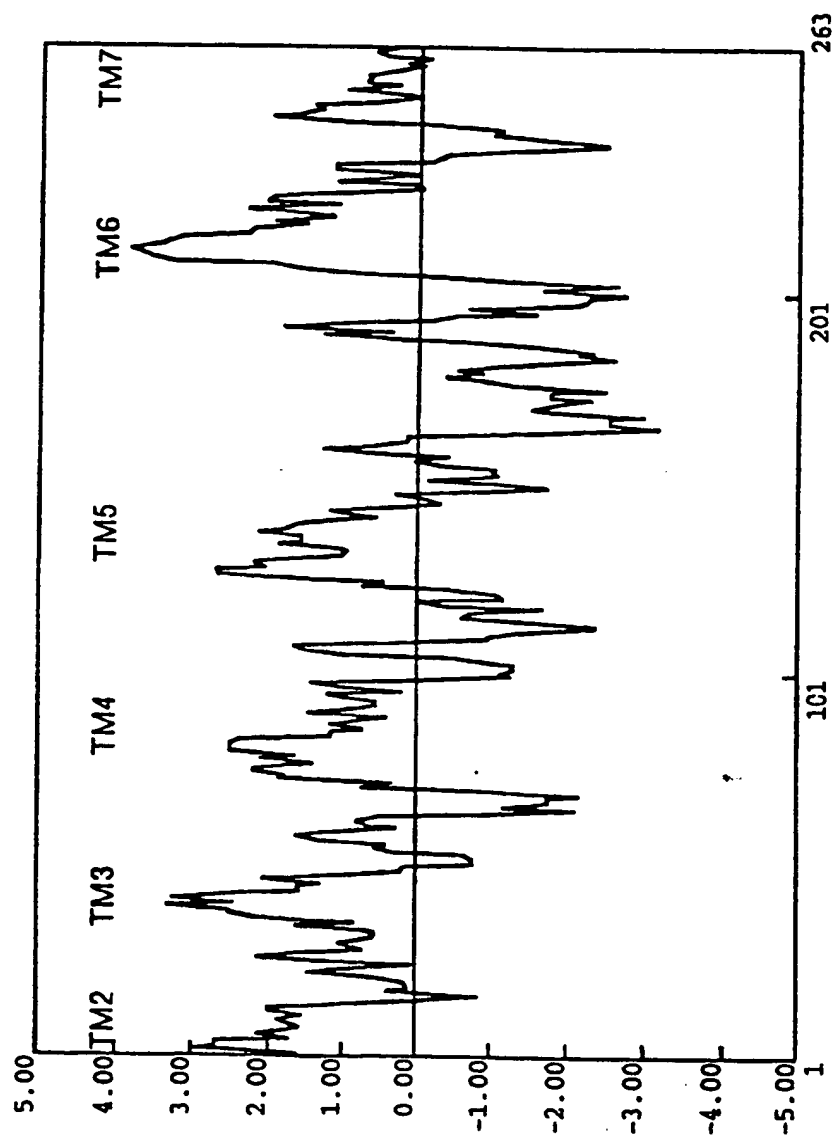
```

-----
Gly Arg Gln Ile Pro Gly Thr Thr Ser Ala Leu Val Arg Asn Trp Lys Arg Pro
      549      558      567      576      585      594
TCA GAC CAG CTG GAC GAC CAG GGC CAG GGC CTG AGC TCA GAG CCC CAG CCC CGG
-----
Ser Asp Gln Leu Asp Asp Gln Gly Gln Gly Leu Ser Ser Glu Pro Gln Pro Arg
      603      612      621      630      639      648
GCC CGC GCC TTC CTG GCC GAG GTG AAA CAG ATG CGA GCC CGG AGG AAG ACG GCC
-----
Ala Arg Ala Phe Leu Ala Glu Val Lys Gln Met Arg Ala Arg Arg Lys Thr Ala
      657      666      675      684      693      702
AAG ATG CTG ATG GTG GTG CTG CTG GTC TTC GCC CTC TGC TAC CTG CCC ATC AGT
-----
Lys Met Leu Met Val Val Leu Leu Val Phe Ala Leu Cys Tyr Leu Pro Ile Ser
      711      720      729      738      747      756
GTC CTC AAC GTC CTC AAG AGG GTC TTC GGG ATG TTC CGC CAA GCC AGC GAC CGA
-----
Val Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Arg Gln Ala Ser Asp Arg
      765      774      783      792      801      810
GAG GCC ATC TAC GCC TGC TTC ACC TTC TCC CAC TGG CTG GTG TAC GCC AAC AGC
-----
Glu Ala Ile Tyr Ala Cys Phe Thr Phe Ser His Trp Leu Val Tyr Ala Asn Ser
      819      828      837
GCC GCC AAT CCC CTC CTC TAC TCC TTC CTC CCT 3'
-----
Ala Ala

```

09033572-031198

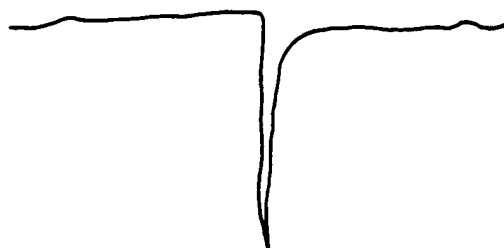
FIGURE 74



7 5 / 7 9

FIGURE 75

10 μ M ATP



100 nA

1 min

09038572-031198

FIGURE 76

h3H2-17(5-3)	1	10	20	30	40	50	50
p3H2-17(5')	1	GTGGGCTGG	TGGGCAACAT	CCTGGCTTCC	TGGCACAAGC	GTGGAGGTGG	50
h3H2-17(5-3)	51	60	70	80	90	100	100
p3H2-17(5')	51	CCGTGCTGCT	TGGGTAGTGT	GTGGAGTCGT	GTGGCTGGCT	GTGACAGCCG	100
h3H2-17(5-3)	101	110	120	130	140	150	150
p3H2-17(5')	101	AGTGGCTGG	CACAGCCATC	TTCGCTGCA	CAGGCAATCA	GGTAAACCG	150
h3H2-17(5-3)	151	160	170	180	190	200	200
p3H2-17(5')	151	ACTGCTGCT	ATGACCTCAG	CCGCGCTGC	CTGGCCACCG	ACTATATGCG	200
h3H2-17(5-3)	201	210	220	230	240	250	250
p3H2-17(5')	201	CTATGGCTAG	GCCTGCTAG	TGATGGCTTT	CTTGGCTGG	TTCATAGGCT	250
h3H2-17(5-3)	251	260	270	280	290	300	300
p3H2-17(5')	251	TGCTGGCTAG	CTATGCTAG	CTGGCTGG	GGTGGCTGG	CCAGGATGGC	300
h3H2-17(5-3)	301	310	320	330	340	350	350
p3H2-17(5')	301	CCAGCAGGTC	CTGTGGCCCA	AGAGCGGCGC	ACCAAGGCGG	CTCGTATGGC	350
h3H2-17(5-3)	351	360	370	380	390	400	400
p3H2-17(5')	351	TGTGGTGGTG	GCAGCTGTCT	TGCCCCCTCTG	CTGGCTGCCT	CTCTAC....	400

1	TGACTCCCTGAACATAGGAAACCCACCTGGGCAGCCATGGAATGGGACAATGGCACAGGC	60
1	MetGluTrpAspAsnGlyThrGly	8
61	CAGGCTCTGGGCTTGCCACCCACCACCTGTGTCTACCGGAGAACTTCAAGCAACTGCTG	120
8	GlnAlaLeuGlyLeuProProThrThrCysValTyrArgGluAsnPheLysGlnLeuLeu	28
121	CTGCCACCTGTGTATTTCGGCGGTGCTGGCGGCTGGCCTGCCGCTGAACATCTGTGTCATT	180
28	LeuProProValTyrSerAlaValLeuAlaAlaGlyLeuProLeuAsnIleCysValIle	48
181	ACCCAGATCTGCACGTCCCGCCGGGCCCTGACCCGCACGGCCGTGTACACCTTAAACCTT	240
48	ThrGlnIleCysThrSerArgArgAlaLeuThrArgThrAlaValTyrThrLeuAsnLeu	68
241	GCTCTGGCTGACCTGCTATATGCCTGCTCCCTGCCCTGCTCATCTACAACATATGCCCAA	300
68	AlaLeuAlaAspLeuLeuTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaGln	88
301	GGTGATCACTGGCCCTTTGGCGAAGTTCGCCTGCCGCTGGTCCGCTTCCTCTTCTATGCC	360
88	GlyAspHisTrpProPheGlyAspPheAlaCysArgLeuValArgPheLeuPheTyrAla	108
361	AACCTGCACGGCAGCATCTCTTCTCTCACCTGCATCAGCTTCCAGCGCTACCTGGGCATC	420
108	AsnLeuHisGlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIle	128
421	TGCCACCCGCTGGCCCCCTGGCACAACGTTGGGGCCGCGGGCTGCCTGGCTAGTGTGT	480
128	CysHisProLeuAlaProTrpHisLysArgGlyGlyArgArgAlaAlaTrpLeuValCys	148
481	GTAACCGTGTGGCTGGCCGTGACAACCCAGTGCCTGCCACAGCCATCTTCGCTGCCACA	540
148	ValThrValTrpLeuAlaValThrThrGlnCysLeuProThrAlaIlePheAlaAlaThr	168
541	GGCATCCAGCGTAACCGCACTGTCTGCTATGACCTCAGCCCGCTGCCCTGGCCACCCAC	600
168	GlyIleGlnArgAsnArgThrValCysTyrAspLeuSerProProAlaLeuAlaThrHis	188
601	TATATGCCCTATGGCATGGCTCTCACTGTCATCGGCTTCCTGCTGCCCTTTGCTGCCCTG	660
188	TyrMetProTyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheAlaAlaLeu	208
661	CTGGCCTGCTACTGTCTCTGGCCTGCCGCTGTGCCGCCAGGATGGCCCGGCAGAGCCT	720
208	LeuAlaCysTyrCysLeuLeuAlaCysArgLeuCysArgGlnAspGlyProAlaGluPro	228
721	GTGGCCCAGGAGCGGCGTGGCAAGGCGGCCCGCATGGCCGTTGGTGGTGGCTGCTGCCTTT	780
228	ValAlaGlnGluArgArgGlyLysAlaAlaArgMetAlaValValValAlaAlaAlaPhe	248
781	GCCATCAGCTTCCTGCCTTTTCACATCACCAGACAGCCTACCTGGCAGTGGGCTCGACG	840
248	AlaIleSerPheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValGlySerThr	268
841	CCGGCGCTCCCTTGCACTGTATTGGAGGCCTTTGCAGCGGCCTACAAGGCACGCGGCCG	900
268	ProGlyValProCysThrValLeuGluAlaPheAlaAlaAlaTyrLysGlyThrArgPro	288
901	TTTGCCAGTGCCAACAGCGTGTGGACCCCATCTCTTCTACTTCACCCAGAAGAAGTTC	960
288	PheAlaSerAlaAsnSerValLeuAspProIleLeuPheTyrPheThrGlnLysLysPhe	308
961	CGCCGCGACCATGAGCTCCTACAGAACTCACAGCCAAATGGCAGAGGCAGGGTCCG	1020
308	ArgArgArgProHisGluLeuLeuGlnLysLeuThrAlaLysTrpGlnArgGlnGlyArg	328
1021	TGA	1023
328	***	329

FIGURE 78

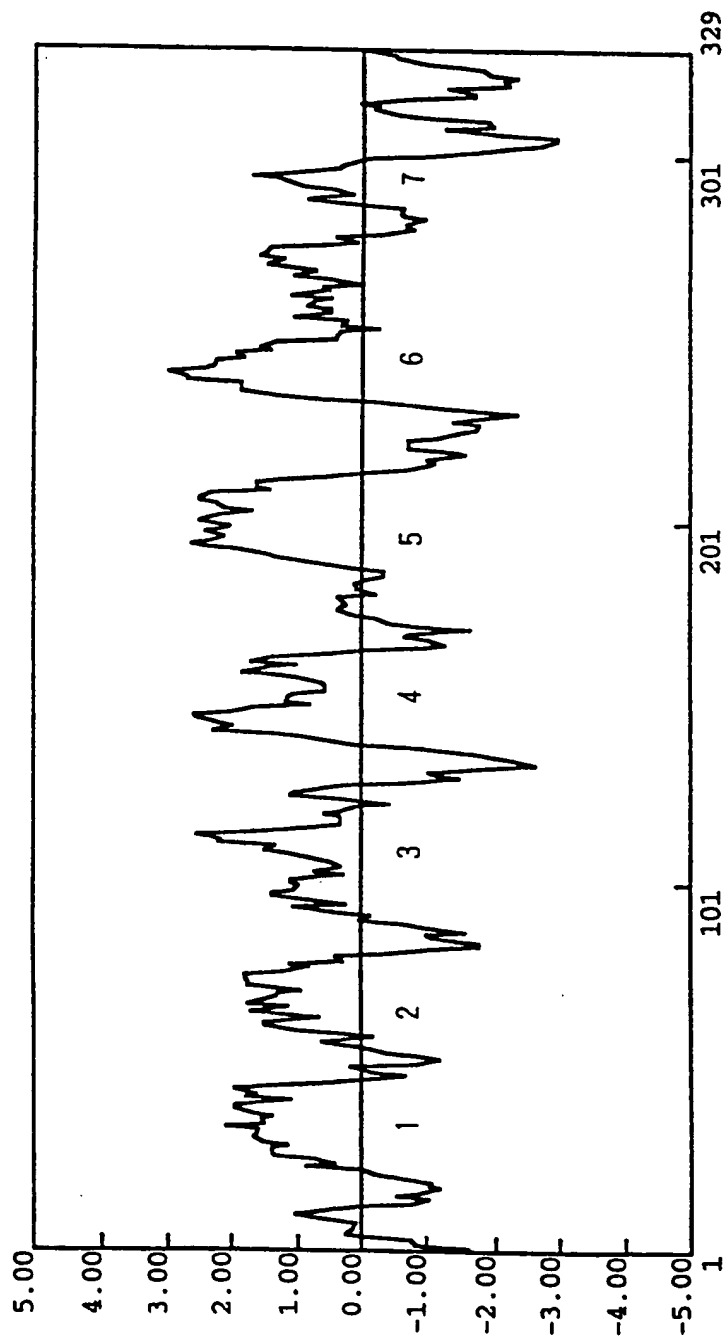


FIGURE 79

human prino, mouseFULL3H2	1	MEWDNGTGOA	10	LGLPPTTCVY	20	RENFQQLLP	30	PVYSVLAAG	40	LPLNICVITG	50
	1	MEQDNGTIOA		PGLPPTTCVY		REDEKRLIT		PVYSVLAAG		LPLNICVITG	50
human prino, mouseFULL3H2	51	ICTSRRALTR	60	TAVVTINLAL	70	ADLVACSLP	80	LLIYNVARGD	90	HWPFQDFACR	100
	51	ICASRRITLTR		SAVVTINLAL		ADLVACSLP		LLIYNVARGD		HWPFQDFACR	100
human prino, mouseFULL3H2	101	LVRFLFYANL	110	HGSILFLTCI	120	SFQRYLGICH	130	PLAPVHKRGG	140	RRAAVLVCVT	150
	101	FVRFLFYANL		HGSILFLTCI		SFQRYLGICH		PLAPVHKRGG		RRAAVLVCVT	150
human prino, mouseFULL3H2	151	VMLAVTQOCL	160	PTAVFAATGI	170	QRNRTVCYDL	180	SPPALATHYM	190	PYGMALTVIG	200
	151	VMLAVTQOCL		PTAVFAATGI		QRNRTVCYDL		SPPALATHYM		PYGMALTVIG	200
human prino, mouseFULL3H2	201	FLLPFAALLA	210	CYCLACRLC	220	RODGPAPVFA	230	QERRGKAARM	240	AVVAVAFAI	250
	201	FLLPFAALLA		CYCLACRLC		RODGPAPVFA		QERRGKAARM		AVVAVAFAI	250
human prino, mouseFULL3H2	251	SFLPEHITKI	260	AVLAVGSTPG	270	VPCIVLEAFA	280	AAKVGTRPFA	290	SANSVLDPIL	300
	251	SFLPEHITKI		AVLAVGSTPG		VPCIVLEAFA		AAKVGTRPFA		SANSVLDPIL	300
human prino, mouseFULL3H2	301	FVFTQAKFRF	310	RPHLLQXLT	320	AKMORQGR*	330	340	350
	301	FVFTQAKFRF		RPHLLQXLT		AKMORQGR*		350